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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
A Geneseq 101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
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1850
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGPPHSGPGGVRVGALLLLG......PVYIVQDGPPQSPPNIYYKV 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			1 1850 1 2 1850 1 3 1850 1	0
4.2		99.7 99.5 99.2	100.0	Ľ
346 1:	334 1	340 155 11	340 18 340 18	ngth DB
7 AAR91930	7 AAW00287 7 AAR92742	8 AAW17081 8 AAW33698 9 AAW46615	8 AAW33699 8 AAW31544 8 AAW10637	н
Elk tyrosine kinas Human cytokine elk	Mouse Eph receptor	EPH family ligand AL-2-long (AL-21) Human transmembran	AL-2-short (AL-2s) Human cytokine Ler NLERK2 ligand for	Description

770	AT.T CMMENTS					
hek-L	AAR71482	16	0	9.2	169.5	50
id sequen	O	19	200	•	172	49
Chicken EPH recept	AAR94767	17	200	•	172	48
Human pancreatic o	AAB54058	21	218	•	172.5	47
	682	20	213	•	175.5	46
acid	10	19	209	9.5	176	45
EPH	476	17	209		176	44
LERK-6 pc	582	20	184		176	43
6 protein.	28	17	184		176	42
vı	AAW02587	17	184		176	4
n hek-L prote	AAR71481	16	238		179	40
Eph transmembrane	AAR82605	16	234		181	39
Drosophila melanog	ABB65548	22	652	٠	182	38
Drosophila melanos	ABB58621	22	652		182	37
Human ephrin B1 C-	AAY71436	21	82		201	36
Human pancreatic c	AAB54187	21	106		202.5	3 5
ephrin E	AAY71437	21	82		204	34
Human peptide	ABG46394	23	136		205.5	ω ω
Peptio	AAM37534	22	136		205.5	32
Human peptide	ABG46524	23	92		284.5	u L
Peptide #11708	AAM37671	22	92		284.5	30
Receptor-type	AAW11307	18	195		431.5	29
Ligand #1 for rec	AAW06333	17	195		431.5	28
Human	AAE24020	23	229		443	27
Murine ephrin B2	AAE24019	23	229		447	26
Ephrin-B1	AAY96781	21	683		452.5	25
Ephrin	AAY96782	21	859		453.5	24
Human eph	AAY71438	21	89		492	23
Ligand for	AAR94656	17	308			22
Ligand #2 for	AAW06334	17	308			21
tor-type	130	18	333			20
LERK-5 cyto	ø	17	333			19
Human hepatoma tra	74	17	333			18
Ligand for recepto	65	17	333		629.5	17
Full length ligand	w	17	333	•		16
Chicken Eph recept	028	17	331	•	4.4	15
transmembi	9	16	346	34.1	631	14
elk-L. Hom	432	19	346	•	632	13
elk ligand	AAW19249	18	346	٠	632	12
Ė		18	346	•	632	11

ALIGNMENTS

AAW33699 standard; Protein; 340 AA.

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RRESULT 1
AAW33699
ID AAW3
XX AAW3
AC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour; rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia; psoriasis; Alzheimer's disease; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW33699;
                                                     WO9740153-A1.
                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                          /note= "signal peptide"
27..340
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                               /note= "extracellular domain"
220..245
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                                                                                                                                                          /note= "hydrophobic transmembrane domain"
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30-OCT-1997

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301

GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

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Best Local Sim
Matches 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL-2 can be used as cognitive enhancer, to enhance learning particularly in dementias or trauma, since they can promote axonal outgrowth and synaptic plasticity, particularly of hippocampal neurons that express AL-2 binding Eph-family receptors and cortical neurons that express AL-2. AL-2 can also be used for wound healing, i.e. accelerating neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids are useful in preparing antibodies that specifically bind to the AL-2 protein. The antibodies and the AL-2 antagonists are useful in diagnosing and treating various neuronal disorders. AL-2 antagonists can be used for modulating angiogenesis. They can also be used for the treatment of tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML), myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ischaemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents, to promote the survival or growth of neurons. They can be used to treat motoneuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and various conditions involving spinal muscular atrophy, or paralysis. AL-2 can be used to treat human neurodegenerative disorders, such as Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome nerve deafness, Menier's disease, and other disorders of the cerebellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-535837/49
N-PSDB; AAV06355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human AL-2 neurotrophic factor and related DNA - used to develop products for, e.g. treating neurologic disorders, angiogenesis disorders, tumours or rheumatoid arthritis or for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Eph-related tyrosine kinase receptor ligand. AL-2 can be administered to patients in whom the nervous system has been damaged by trauma, surgery, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Fig 2A-B; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-1996;
                      301
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                                                                                                                                                                                                                                                                                                                           LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLICDRPDLDLRFTIKFQEY 120
                                                                                                                                                                                                                                                                                                                                                                                                    MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSPVYMNSANKRFQAEGGYVLYPQIGDRLDL 60
GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                                                                                                                                                                                                                                                                                                                             MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
                                                                                     GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG
                                                                                                                                                            VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                                     SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
                                                                                                                                                                                                                                                          SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
                                                                                                                                         VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             psoriasis and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1850; DB 18;
Pred. No. 2.9e-143;
); Mismatches 0;
                      340
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ARBSULT 2
ARASULT 2
ARASUL
This protein sequence comprises a novel human cytokine designated Lerk-8. The amino acid sequence was deduced from a human foetal brain cDNA clone (see AAT89519). Lerk-8 binds to the cell surface receptors hek and elk, which are members of the eph/elk family of receptor tyrosine kinases. Lerk-8 polypeptides, especially soluble polypeptides comprising amino acid residues -27 to 142-197 of the cfull-length protein, can be expressed in transformed host cells. These polypeptides can be used to purify hek or elk proteins, and to purify or identify cells that express hek or elk proteins, and to purify or identify cells that express hek or elk on the surface. Such cells can be used in various in vitro studies or in vivo procedures, e.g. neural cells expressing elk can be administered to a mammal afflicted with a neurodegenerative disorder. The Lerk-8 polypeptides can also be used to deliver diagnostic or therapeutic agents to these cells (e.g. leukaemia cells). The Lerk-8 DNA and polypeptides can also be used to: treat disorders mediated by such as injury to neural tissue or neurologic disease; to promote can and for wound healing or stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase;
ligand; neurodegenerative disease; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated cytokine, Lerk-8 - binds to the hek and elk receptor tyrosine kinases, used to develop products for diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-503043/46.
N-PSDB; AAT89519.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-1996;
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28..224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "residue 325 is Leu in Lerk-8 variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252..340
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Best Local S
Matches 340
                                        05-FEB-1996;
20-JUL-1995;
27-NOV-1995;
22-DEC-1995;
  Nicola NA;
                                                                                                                                                                                                                                                                                    LERK; ligand for eph-related kinase; ERK; NLERK2; receptor protein tyrosine kinase; cell proliferation; cell differentiation; cell survival; nerve cell.
                                                                                                                  06-FEB-1997.
                                                                                                                                     WO9704091-A1
                                                                                                                                                                     Modified-site
                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                            AAW10637 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neovascularisation
                                                                                             19-JUL-1996;
                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                             NLERK2 ligand for eph-related kinase.
                                                                                                                                                                                                                                                                                                                                                   23-JUN-1997 (first entry)
                      (AMRA-) AMRAD
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les 340; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
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                     OPERATIONS PTY
                                        96AU-0007890.
95AU-0004263.
95AU-0006847.
95AU-0007299.
                                                                                            96WO-AU00460
                                                                                                                                                                                          30..340
/label= Mat_protein
227..251
                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                      /label= N-glycosylation_site
                                                                                                                                                                                                                     /label= Sig_peptide
                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                            Protein; 340
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                     LTD
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Pred. No. 2.9e-143;
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RESULT 4
AAW17081
ID AAW1
XX AAW1
AC AAW1
XC AAW1
XC EPH
XX EF1-
XW Ef1-
XW 1iga
XX Homo
XX Homo
XX Homo
FT Pept
FT Prot
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Best Local S
Matches 340
                                                                                                              Efl-6; I
ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A novel human ligand for eph-related kinase (LERK) is designated MLERK2 (AAW10637). It is encoded by a cDNA clone (AAT60966) obtd. from a human foetal brain cDNA library. The novel receptor ligand can be expressed in transformed host cells and used in methods for regulating the development, maintenance or regeneration of different cells (e.g. neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be used to treat injury, disease or abnormality in the nervous system, and membrane-bound NLERK2 to modulate proliferation, different or survival e.g. in grafting procedures or transplantation. NLERK2 can also be used to raise antibodies for use in immunotherapy, and to detect anti-NLERK2 antibodies that may occur in some autoimmune diseases.
                                                                               Homo sapiens
                                                                                                                                                             EPH family
                                                                                                                                                                                            09-AUG-1997 (first entry)
                                                                                                                                                                                                                             AAW17081;
                                                                                                                                                                                                                                                          AAW17081 standard; Protein;
                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid mol. encoding ligand for eph-related kinase - of treatment of, pref. neuronal, cells to increase surviva. proliferation and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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N-PSDB; AAT60966.
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hes 340;
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                                                                                                            Eph; Elk; receptor tyrosine kinase; signal transduction; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 100.0%; Score 1850; DB 18; Similarity 100.0%; Pred. No. 2.9e-143; 40; Conservative 0; Mismatches 0;
                                                                                                                                                             ligand Ef1-6.
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 1..24
/label= Sig_peptide
25..340
                                              Location/Qualifiers
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Best Local S
Matches 339
                                                                                                                                                                                                                                                                                                                                                                                                                    A novel ligand (AAW17081), designated Ef1-6 (or Eph transmembrane tyrosine kinase family ligand 6), binds to the Elk, Nuk/Cek5, Hek and Sek1 receptors on cells. Its amino acid sequence was deduced from a human frontal cortex cDNA clone (AAT69808). Recombinant Elf-6, truncated soluble polypeptides comprising the extracellular domain of Elf-6, and Ef1-6 ligandbodies comprising soluble Ef1-6 and the Fc portion of IgG can be expressed in host cells. These can be used to support neuronal and other Eph receptor-bearing cell populations for treatment of neurological disorders, in drug screening and to raise diagnostic
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding Efl-6 ligand protein - used for promoting growth and proliferation of neuronal cells and in drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis
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                                                                                                                                                                                                                                 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
                    GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                   GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG
                                                                                                          VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                   VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                              SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP
                                                                                                                                                                                       SPNIMGHEFRSHHDYYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGAVFRKP 180
                                                                                                                                                                                                                                                                        MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                                                                                                                                                                                                                                                                                                             339;
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                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT69808.
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                                                                                                                                                                                                                                                                                                                             Conservative
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225..249
/label= Transmembrane_domain
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Pred. No. 9e-143;
0; Mismatches 1;
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                        340
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RESULT 5
AAW33698
ID AAW3
XX

AAW33698 standard; Protein; 455

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Query Match Best Local

Similarity

99.5%;

Score 1841; DB 18; Pred. No. 2.2e-142;

Length 455;

Sequence

455 AA;

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CC tyrosine kinase receptor ligand. AL-2 can be administered to patients in CC whom the nervous system has been damaged by trauma, surgery, stroke, CC ischaemia, infection, metabolic disease, nutritional deficiency, CC malignancy, or toxic agents, to promote the survival or growth of CC amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and CC amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and CC amyotrophic lateral sclerosis, thou scular atrophy, or paralysis. AL-2 CC can be used to treat human neurodegenerative disorders such as CC Alzheimer's disease, Parkinson's disease, apilepsy, demyelinating CC diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome, CC AL-2 can be used as cognitive enhancer, to enhance learning particularly in dementias or trauma, since they can promote axonal outgrowth and CC synaptic plasticity, particularly of hippocampal neurons that express CAL-2. AL-2 can also be used for wound healing, i.e. accelerating CC neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids and treating various neuronal disorders. AL-2 antagonists are useful in diagnosing cortein. The antibodies and the AL-2 antagonists are useful in diagnosing cortein. The antibodies and the AL-2 antagonists are useful in diagnosing and treating various neuronal disorders. AL-2 antagonists can be used for modulating angiogenesis. They can also be used for the treatment of cumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML), chronic myeloid leukaemia (CML), chronic myeloid leukaemia and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human AL-2 neurotrophic factor and related DNA - used to develop products for, e.g. treating neurologic disorders, angiogenesis disorders, tumours or rheumatoid arthritis or for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL-21; AL-2; AL-2-long; human; treatment; neurological disorder; tumour; rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia; psoriasis; Alzheimer's disease; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is a AL-2-long (AL-21) protein. The AL-2 is tyrosine kinase receptor ligand. AL-2 can be admit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV06354.
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                         Modulating transmembrane ligand for an Elk-related receptor tyrosine kinase - by formation of a complex between an oligomerised Elk-related receptor tyrosine kinase and a transmembrane ligand
                                                                                                                                   N-PSDB; AAV16097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction; organogenesis; oncogenesis; tumour; neurological disorder; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This polypeptide comprises human Elk-L3, a transmembrane ligand of Elk-related receptor tyrosine kinase (ERRTK). A novel method of modulating the biological activity of, or for affecting a pathway regulated by, a transmembrane ligand for an ERRTK in a cell expressing the transmembrane ligand comprises forming a complex between a purified and isolated oligomerised ERRTK, or an isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shy Drager's syndrome, cerebellar atrophy, pe
                                                                                                                              19-JAN-1997
                                                                                                                                                                       AAW00287;
                                                                                                                                                                                                               AAW00287 standard;
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                                                                                                                                                                                                                                                                                                                                                GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG
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                                                                                                                                                                                                                                                                                                                                                                                                        GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG
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                                                                                  receptor ligand
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                                                                                                                            (first entry)
                                                                                                                                                                                                               Protein; 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peripheral nerve damage,
                                                                                  ELF-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1836; DB 1
Pred. No. 4e-142;
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Query Match
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Matches 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eph receptor ligand, ELF-2, and DNA encoding it - used to prevent neurological diseases, and to modulate binding of Eph receptor, e.g. to prevent or treat tumour formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bergemann AD,
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                                                                                                                                                                                                                                                                                                                                                                                                                       GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALLLIGVIGIVSGISLEPVYWNSANKRFQAEGGYVLYPQIGDRIDLICPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                          GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 131
                                                                                                                                                                                                                                                                                                                                                                       PNYEFYKLYLVGGAQGRRCEAPPAPNLLLITCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1996-433391/43.
                                   YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                   KYRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
                                                                                                                               WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                       GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
                                                                                                                                                                                                               GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                                                                                                                                                      DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 191
                                                                                                                                                                                                                                                                                                DYYLIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
           YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
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31..15
/label= Receptor_binding_site
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/label= Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 637.5; DB 17;
Pred. No. 4.6e-44;
9; Mismatches 129;
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ELF-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The DNA is used to produce recombinant ligands; for tissue-
specific typing (partic. as a marker for breast cancer) and as a
marker for human chromosome 13. The ligands (partic. in soluble
form) are used to activate the tyrosine kinase domain of the
Htk receptor, i.e. to stimulate or inhibit growth, differentiation,
and/or activation of cells conty. the receptor, e.g. treatment
of neurodegenerative diseases, since they are strongly expressed
in the cerebral cortex, hippocampus, striatum and cerebellum.
The ligands are also useful as a control or standard in assays,
for generation of antibodies, as a mol. wt. marker, for growth
in vitro of Htk-receptor positive cells, as research agent,
in screening, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse (AAT16470) and human (AAT16471) Htk ligand which activate, the Htk receptor, have been identified in a v tissues using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the murine Htk ligand protein signal peptide cleavage is 34 kD with an estimated pI of the murine and human ligands show 96% homology at the a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ligand for the hepatoma trans-membrane kinase receptor - stimulating and inhibiting cells carrying the receptor, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-105907/11.
N-PSDB; AAT16470.
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                                     DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                        GALLLIGVIGIVSGISLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN
                                                                                                                                                                                  PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                               GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
                                                                                                                                                                                                                                                                                                                                                                            139;
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                                                                                                                                                                                                                                                                                                                                                                        34.5%; Score 637.5; DB 1
42.1%; Pred. No. 4.6e-44;
tive 49; Mismatches 129
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                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 145; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA encoding ligand for elk tyrosine kinase receptor related polypeptides, vectors, antibodies and probes, use in studying cell differentiation or growth
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                          The sequence is that of the elk-L protein able to bind a tyrosine kinase receptor. The DNA may be incorporated i which can used to study the role of elk and its ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 30; 35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baum PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vectors; elk-L protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elk tyrosine kinase receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AARS5059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR55059
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     64
                                                62
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                            CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
                                                                                                                                             PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANXRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1994-183415/22.
DB; AAQ65486.
                                                                                              PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KYRRRHRKHSPOHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR----TADSVFCPH
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                                                                                                                                                                                                                                                                                                                                           and differentiation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beckmann MP,
                                                                                                                                                                                                                                                                                            346
                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "mature elk-L protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                  34.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            elk; ligands; cell growth; differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyman
                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346
                                                                                                                                                                                                                  Score 632;
Pred. No. 1
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                                                                                                                                                                                                                                       Length 346;
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d into vectors
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RESULT 10
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The present sequence is the human cytokine elk-ligand (elk-L), which binds a member of the tyrosine kinase receptor family. Elk-L exhibits neurotrophic and neuroprotective properties, and has a calculated mol. wt. 35180 daltons and a pI of 9.006. The elk-L cDNA, isolated from a human placental cDNA library, can be radiolabelled and used as a probe for isolating other mammalian elk-L cDNA. Elk-L can be used to treat neural tissue disorders,
                                                                                                                                                                     WPI; 1996-229866/23.
N-PSDB; AAT28770.
                                                                                                                                                                                                                                                             15-MAR-1994;
13-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; elk-ligand; elk-L; tyrosine kinase receptor; neurotrophic; neuroprotective; placenta; radiolabelled probe; treatment, neural tissue; excito-toxicity; injury; disorder; neural culture reagent; immunogenic fragment; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR91930 standard;
                                                                                                     Claim 1; Columns 27-30; 18pp; English.
                                                                                                                                probe to
                                                                                                                                                                                                           Baum
                                                                                                                                                                                                                                                                                                   13-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytokine elk-ligand (elk-L).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                              coding for neurotrophic human elk ligand sequences
                                                                                                                                                                                                           PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
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                                                                                                                                                                                                           Beckmann
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92US-0977693.
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/label= sig_peptide
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                                                                                                                                            cytokine - useful
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Best Loca
Matches
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                  Cleavage-site
                                                   Cleavage-site
                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                  extracellular
                                                                                                                                                                                                                                                                                                                                                                                                Human; elk-L;
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                                                                                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANIYYKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LLLLGVAGAGGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                 elk-L
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                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                cytokine;
domain; i
 /note= "K
267..268
/note= "K
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25..237
/note= "
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25..34
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                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                    . 267
                                                                                                                                                                                                                                                                                                                                                                              e; ligand; tyrosine kinase receptor; fusion protein;
immunoglobulin; neurological disease.
                                                                 "Asn
                                                                                                                                                                    "extracellular domain; this region i generate a fusion protein with the of the human immunoglobulin G1"
                                                                                                                                                                                                                                         "mature protein"
                                                                                                                                                                                                                                                                          "signal
                                                                                                                                        "transmembrane domain"
                                                                                                      "intracellular
                                    "KEX2
   "KEX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
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Pred. No. 1.3e-43;
8; Mismatches 116;
                                protease cleavage site"
 protease
                                                                                                                                                                                                                                                                          peptide"
                                                                   N-glycosylated'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MCWRRRRAKPSESRHPGPGSFGRGGSLGL
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 cleavage site'
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                                                                                                                                                                                        is used
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                                                                                                                                                                                        portion
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ID AAW1
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Matches
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Best Local Similarity
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13-NOV-1992;
02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the amino acid sequence of the human elk-L protein, a new cytokine that is the ligand for the elk tyrosine kinase receptor. The extracellular domain of the protein (amino acids 1-213) is used to generate a fusion protein comprising the Pc polypeptide of the human immunoglobulin G1 (extending from the hinge region to the C-terminus). The fusion protein (which has the same activities as the natural elk-L protein) has neuroprotective and neurotrophic activity so is potential useful for treating a wide range of neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soluble fusion proteins of human elk-ligand fragment - and their dimers and oligomers, uneuro-protectants and neurotrophic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
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DB; AAT97976.
                                                                                                                                                                                                                                                                                                                                                                                                  CPRARPPGPHSSPNYBPYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                                   PNIYYKV
                                                                       STLASPKGGSGTAGTEPSDITIPLR
                                                                                                                                                                                                                                                                                             PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGYCRTRTMKIIMKVGQDPNAVTPEQLTT
                                                                                                                                                                                                                                                                                                                               PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV
                                                                                                                                                                                                                                                                                                                                                                   CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQETRFTIKFQEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                PĠQRWLĠKWĹVAMVVWALCRĹATPLAKNĹĔPVSWSŚLNPKFLSGKĠLVTYPKIGDKLDII
                                                                                                                                              GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ
                                                                                                                                                                                                                      SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD
                                                                                                                                                                                                                                                        SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145;
                                                                                                       -GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
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                                                                                                                                                                                  -LLLIGVAGAGGA---
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92US-0977693.
95US-0460741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 632; DB 18;
Pred. No. 1.3e-43;
8; Mismatches 116;
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                                                                         ---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
                                                                                                                                                                                -----MCWRRRAKPSESRHPGPGSFGRGGSLGL
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13-NOV-1992;
01-JUN-1995;
                                                                                                                                                                                                                                                                The present sequence is a human elk ligand (elk-I) protein, which binds elk, has a calculated molecular weight of 35180 and an isoelectric point of 9.006. Elk-I is a cytokine that can be used to test cells for elk expression, measure the biological activity of elk, purify elk by affinity chromatography and as a neuroprotective agent to treat diabetic, hereditary and nutritional neuropathies and neurodegenerative diseases. It may also be added to tissue cultures to prolong the life of neurons. The elk-L cDNA was isolated from a human placental cDNA library, and is present as a cDNA insert in the recombinant vector deposited in strain
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human elk ligand protein - as neuro-protective agent
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Columns 29-32; 18pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-271366/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; elk; ligand; elk-L; cytokine; testing; measuring; purification; neuroprotection; treatment; diabetic; hereditary; nutritional; neuropathy; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human elk ligand protien.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                         119
                                                   122
 182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
                                                                             64
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                                                                                                                                                                                           Local Similarity
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                                               PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                          CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
                                                                                      CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR,
                        PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                                                                                                             PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                   PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                              145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     culture.
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                                                                                                                                                                                                                                346 AA;
                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0213403.
92US-0977693.
95US-0458077.
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25..346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= mat_peptide
                                                                                                                                                                                          34.2%;
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                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  for diagnostic
                                                                                                                                                                                          Score 632; DB 18;
Pred. No. 1.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                             English.
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                                                                                                                                                                              Mismatches
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                                                                                                                                                                              116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutic
                                                                                                                                                                                                    Length 346;
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   use,
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RESULT 13
AAW44323
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AC AAW44
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13-NOV-1992;
02-JUN-1995;
12-NOV-1996;
                                               The present sequence represents human elk-L (elk ligand). The present invention describes antibodies to elk-L polypeptides. The elk-L protein is known to be neuroprotective exhibiting its effect through a trophic mechanism. Examples of diseases that may be treated with elk-L include neuropathles e.g. diabetic, hereditary and nutritional neuropathies, neurodegenerative diseases and other diseases characterised by loss of function or degeneration of neurons.
  Sequence
                                                                                                                                                                                                                                                             Claim 1; Column 31-32; 17pp; English.
                                                                                                                                                                                                                                                                                                            Antibodies to elk ligand polypeptides - bind receptors, useful for treating neural disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; elk-L; el
tyrosine kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                1998-206621/18.
DB; AAV15226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANIYYKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beckmann
  346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elk ligand;
se receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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92US-0977693.
95US-0460741.
96US-0747240.
  B
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25..346
/label= elk-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytokine; antibody; cell surface receptor; neural disease; trophic mechanism.
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                                                                                                                                                                                                                                                                                                                                           to tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GASGGSSGDPD
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Query Match 34.:
Best Local Similarity 39.:
Matches 145; Conservative

34.2%;

48;

Score 632; DB 19; Pred. No. 1.3e-43; 8; Mismatches 116;

Length 346; Indels

58,

Gaps

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RESULT 14
AAR82606
ID AAR82
XX AAR82
XX AAR82
XX 16-MA
DT 16-MA
DT 16-MA
DT 16-MA
C Efl-2
KW neuro
XX Homo
XX 
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                                                                                                                                                                                                                                       21-OCT-1994;
04-APR-1994;
12-APR-1994;
01-SEP-1994;
                                                                                                                  Aldrich TH,
Yancopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Peptide
  neurological disorders
                                                                                                                                                                                                                                                                                                                                                              04-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                            12-0CT-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Efl-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand; neurological disorder; identification; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eph transmembrane tyrosine kinase family ligand, Efl-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR82606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR82606 standard;
                      Ligands which bind Eph
                                                                         WPI; 1995-358635/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                            (REGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
                                                                                                                                                                                            REGENERON
                                                                                                                    Davis S, GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·LLLLGVAGAGGA--------MCWRRRAKPSESRHPGPGSFGRGGSLGL
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94US-0222075.
94US-0229402.
94US-0299567.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= signal_peptide
238..263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "borders main conserved regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= transmembrane_domain
                                                                                                                                                                                            PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                      family receptors - used
                                                                                                                                           Gale N,
                                                                                                                                                                                            INC
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                                                                                                                                           Goldfarb M,
                                                                                                                                           Maisonpierre
                         ä
                         the diagnosis
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WPI; 1996-433391/43 N-PSDB; AAT40231.

Bergemann AD,

Flanagan

ĮĢ,

HARVARD

COLLEGE

27-FEB-1995; 23-FEB-1996; 06-SEP-1996.

95US-0395415 96WO-US02673 Gallus sp. diagnosis;

gene

therapy.

WO9626958-A2

Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction; organogenesis; oncogenesis; tumour; neurological disorder;

Chicken Eph receptor ligand

ELF-2.

19-JAN-1997

(first

entry)

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AAWOO288
ID AAWOO
XX AAWOO
AC 
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW00288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVLLLKLRKRHRKHTQQ-------RAAALSLSTLASPKGGSGTAGTEPSDIIIPLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----MCWRRRAKPSESRHPGPGSFGRGGSLGL----GGGGGMGPREAEPGELGIALRGG
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Pred. No. 1.6e-43;
4; Mismatches 105;
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RESULT 16
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Best Local Sim
Matches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicken Eph receptor ligand ELF-2 (AAW00288) is a ligand important in cellular communication during pattern formation. It is strongly expressed in the anterior hindbrain and newly-forming semites of embryos at the early organogenesis stage of development. Its amino acid sequence was deduced from a cDNA clone (AAT40231) isolated from a chicken cDNA library. The ELF-2 ligands can be used to alter neurological development, oncogenesis and growth regulation, to modulate binding of ELF-2 to the Eph receptor, and in diagnostic
                                                                                                                                                                                                                                                   Full length
                                                                                                                                                                                                                                                                                  17-JAN-1997
                                                                                                                                                                                                                                                                                                               AAW06337;
                                                                                                                                                                                                                                                                                                                                             AAW06337 standard;
                  23-JUL-1996.
                                               JP08188596-A.
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                  Receptor-type tyrosine kinase; ligand; coomassie staining; PAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eph receptor ligand, ELF-2, and DNA encoding it - used to prevent neurological diseases, and to modulate binding of Eph receptor, e.g. to prevent or treat tumour formation.
                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Fig 2A-D; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALLLLGVLGLVSGLSLEPVYWNSANKRPQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                       CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSDNLWGHBFRSHH 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLKYRRRHRKHSPOHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTNGKSSTTSPFVKDHSGSSTDG--SKAGHSSILGSEVALFAGIASGCIIFIVIIITLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYYVISTSNGSLEGLNNQEGGVCQTKTMKILMKVGQDPNSAGLPR---SSDPTKRPEQEA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMER----- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYEYYKVYMVDKDQADSCAIRKDNTPLLNCAKPDQDVKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALMVIMRTALAKSIVIDPIYMNSSNPKFLPGQGLVLYPQIGDKLDIICPKV---DSKTA 70
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                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                             Protein;
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40.5%; Pred. No. 1.7e-43;
tive 53; Mismatches 124;
                                                                                                         "signal peptide"
                                                                           "receptor-type tyrosine kinase binding
                                                                                                                                                                                                                                               receptor-type tyrosine kinase protein.
                                                                                                                                                                                                                                                                                                                                             333
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ELF-2
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                                                                             protein"
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ARSULT 17
AAR94655
ID 9AR94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                             18-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the full length receptor-type tyrosine kinase protein binding ligand of the invention (also see AAW06333 and AAW06334). The mature protein contained within this sequence contains the N-terminal fragment represented by AAW06332. The proteins of the invention have a molecular weight of 23500 (plus or minus 1500) Da, and are positive for Coomassie staining and PAS staining. The proteins of the invention bind to the fragment of this protein sequence represented by AAW06330. The proteins of the invention are new ligands of receptor-type tyrosine kinases, and can be prepared by standard
                                                               haematopoietic
                                                                            Receptor type tyrosine kinase; TK; ligand; differentiation;
                                                                                                          Ligand for receptor type tyrosine kinase (TK).
                                                                                                                                                                                                       AAR94655 standard; Protein; 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New ligand for receptor type tyrosine kinase - ha kilo:dalton(s) and is positive for Coomassie and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-388601/39.
N-PSDB; AAT42594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-1994;
19-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 11; Page 44-46; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JAN-1995;
                                                                                                                                                                                                                                                                                       304
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                                                                                                                                                                                                                                                                                                                                                                                                                                          191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 GQYBYYKVYMYDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                                                                                                                                                                                                                                                               WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVERKPVSEMEMER-DR
                                                                                                                                                                                                                                                                                     YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                                                                                                                                                                                                                 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH
                                                                                                                                                                                                                                                                                                                                                                                                              GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDXLDIICPKV---DSKTV
                                                                                                                                                                                                                                                                                                                 YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYYTTSTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95JP-0003677.
                                                               cell; tyrosine; bone marrow;
                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 629.5; DB 17;
Pred. No. 2.1e-43;
2; Mismatches 130;
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                                                               leukaemia
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W09611212-A1 Homo sapiens.

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RESULT 18
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ID AAR92
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AC AAR92
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Best Local Sim
Matches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A ligand polypeptide which binds to the extracellular part of a specific receptor-type tyrosine kinase and induces phosphorylation of tyrosine within the cell can be used in the study of the differentiation of blood cells such as the haematopoietic stem cells; of disease processes such as leukaemia, and of the biology of bone marrow transplantation. The ligand plays a role in the differentiation process and the specific ligand target is expressed differentiation process and the specific ligand target is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ligand peptide binding intracellular tyrosine undifferentiated blood
 Hepatoma transmembrane kinase;
                           Human hepatoma transmembrane kinase receptor ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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07-OCT-1994;
                                                                                                         AAR92743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in undifferentiated blood cells.
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                                                                                                                                                                                                                                                      WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGRGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                                                 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAĞIÁSĞCIIFIVIIITLVVLLL
                                                                                                                                                                                                                                                                                                         GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                                                                                                                                                                                                                                     DYYTTSTSNGSLEGIDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN
                                                                                                                                                                                                                                                                                                                                                               DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                                                                                                          GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH
                                                                                                                                                                                                                                                                                                                                                                                                                                             GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
                                                                                                                                                                         YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
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                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 163-164; 193pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                      (first
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94JP-0244433.
94JP-0262882.
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                                                                                                       Protein; 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to receptor-type tyrosine kinase - enhances phosphorylation, useful for investigation of cell behaviour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 629.5; DB 1
Pred. No. 2.1e-43;
2; Mismatches 130
 Htk;
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 receptor; ligand
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specific typing (partic. as a marker for breast cancer) and as a
marker for human chromosome 13. The ligands (partic. in soluble
form) are used to activate the tyrosine kinase domain of the
Htk receptor, i.e. to stimulate or inhibit growth, differentiation,
and/or activation of cells contg. the receptor, e.g. treatment
of neurodegenerative diseases, since they are strongly expressed
in the cerebral cortex, hippocampus, striatum and cerebellum.
The ligands are also useful as a control or standard in assays,
for generation of antibodies, as a mol. wt. marker, for growth
in vitro of Htk-receptor positive cells, as research agent,
in screening, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse (AAT16470) and human (AAT16471) Htk ligand which bind to, a activate, the Htk receptor, have been identified in a variety of tissues using a soluble Htk-Fc fusion protein.

The predicted mol.wt. of the murine Htk ligand protein following signal peptide cleavage is 34 kD with an estimated pI of 8.9. The murine and human ligands show 96% homology at the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Fig 2(A-B); 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating neuro-degenerative disease
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YEKVSGDYGHPYYIVQDGPPQSPPNIYYKV
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                                                                                                                                                                                                                                                                                                                                                                     GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                    KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIPLR---TADSVFCPH
                                                                                                                       GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFÅGIÅSGCIIFIVIIITLVVLLL
                                                                                                                                                      GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                                                                                                                                                                GOYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK
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                                                                                     WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                            DYYIISTSNGSLEGIDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN
                                                                                                                                                                                                                             DYYITATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
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Pred. No. 2.1e-43;
2; Mismatches 130
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                        130;
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304 YEKVSGDYGHPVYIVQEMPPQSPANIYYKV

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RESULT 19
AAR89287
ID AAR89287
ID AAR89287
AC AAR89
AC AA
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   N-PSDB; AAQ99288
                     WPI; 1996-097585/10
                                                           Cerretti DP,
                                                                                                                                  08-JUL-1994;
                                                                                                                                                                     06-JUL-1995;
                                                                                                                                                                                                           25-JAN-1996.
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                                                         Reddy P;
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                                                                                              CORP.
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257..258
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/note= "KEX2 protease processing site"
                                                                                                                                                                                                                                                                                                     /note=
276..2
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GenBank L13189 translation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cytoplasmic domain"
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                   Key
Peptide
                                                                                                                                                                                                                                                                                AAW11308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
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Best Local Similarity Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a full-length LERX-5 cytokine, which binds elk and hek receptor protein-tyrosine-kinases (members of the eph/elk family), and expressed from a gene isolated by amplification with primers specific for a chromosome-13 expressed sequence tag, GenBank L13189, from a human T-lymphocyte leukaemia CCRF-HSB-2 (ATCC CCL 120.1) cell line, followed by cDNA probe screening of a human fetal brain cDNA library in phage lambda-gtl0. A truncated soluble form may also be produced. The protein may be produced as a recombinant fusion protein or dimer with an antibody Fc fragment or e.g. a FLAG affinity tail (R89288). LERK-5 may be used in binding assays to detect elk- or hek-expressing cells, to measure elk or hek activity, as a drug delivery for elk or hek receptor-specific cell therefore, e.g. for delivery of cytostatic agents in leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding LERK-5 cytokine capable of binding elk and hek - used as carrier to deliver attached (anti-leukaemic) agents to cells bearing elk or hek, i.e. human leukaemia cell lines JM and LK63
                                                                         14 GALLLIGVIGIVSGISLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLICPRARPPGPHSS
GVLMVLCRTAISKSIVLEPIYMNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 31-32; 40pp; English.
                                                                                                                                                                                                                                                                                                  333 AA;
                                                                                                                                                   Conservative
                                                                                                                                                                              34.0%;
                                                                                                                                                   52; Mismatches 130;
                                                                                                                                                                                  Score 629.5; DB:
Pred. No. 2.1e-43,
                                                                                                                                                                                                                        DB 17;
                                                                                                                                                   Indels 13;
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                                                                                                                                               Gaps
       70
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Receptor-type tyrosine kinase; LPM medium; ligand; autophosphorylation; insect cell; animal cell; growth promoter; undifferentiated cell; insulin; interleukin; fibroblast growth factor; hapatocyte growth factor nerve growth factor; interferon-gamma; tumour necrosis factor; inducer. 21-MAR-1997 Receptor-type AAW11308 standard; (first entry) tyrosine kinase #4. protein; 333 \$

310

250 250 190

133

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Homo sapiens /label= signal peptide Location/Qualifiers

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RESULT 21
AAW06334
ID AAW06
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AC AAW06
AC TAW06
DT 17-JP
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Best Local Similarity
Matches 135; Conserv
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                 Ligand #2
                                                      17-JAN-1997
                                                                                        AAW06334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GALLLLGVIGIVSGISLEPVYWNSANKRFQAEGGYYLYPQIGDRLDLLCPRARPPGPHSS 73
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                                                                                                                                                                                                                 YEKVSGDYGHPVYIVQEMPPQSPANIYYKV
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                 for receptor-type tyrosine kinase protein.
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                                                      (first
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Pred. No. 2.1e-43;
2; Mismatches 130;
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   RESULT 22
AAR94656
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AC AAR94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW06333 and AAW06334 represent receptor-type tyrosine kinase receptor binding ligands of the invention. These sequences both have the N-terminal sequence represented by AAW06332. The ligands of the invention recognise the fragment of the receptor type kinase receptor represented by AAW06330 (see AAW06331 for full length sequence). The proteins of the invention have a molecular weight of 23500 (plus or minus 1500) Da, and are positive for Coomassie staining and PAS staining. The protein is a new ligand of receptor-type tyrosine kinases, and can be prepared by standard recombinant techniques.
   Ligand for
                                                                                                         AAR94656 standard; Protein; 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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19-OCT-1994;
                                       18-OCT-1996
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kilo:dalton(s) and is positive for Coomassie and PAS staining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 DRCTIKKENTPLLNCAKPDODIKFTIKFOEFSPNLWGLEFOKNKDYYLISTSNGSLEGLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 LEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DRGAAHSLEPGKENLPGD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQA 61
                                                                                                                                                                                                                                                                        LSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQ
                                                                                                                                                                                                                                                                                                       GSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQ
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   receptor type tyrosine kinase
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                                     (first entry)
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94JP-0253848.
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Pred. No. 1.2e-42;
8; Mismatches 121;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A ligand polypeptide which binds to the extracellular part of a specific receptor-type tyrosine kinase and induces phosphorylation of tyrosine within the cell can be used in the study of the differentiation of blood cells such as the haematopoietic stem cells; of disease processes such as leukaemia, and of the biology of bone marrow transplantation. The ligand plays a role in the differentiation process and the specific ligand target is expressed in undifferentiated blood cells.
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07-OCT-1994;
26-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligand peptide binding to receptor-type tyrosine kinase - enhances intracellular tyrosine phosphorylation, useful for investigation oundifferentiated blood cell behaviour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor type tyrosine kinase; TK; ligand; differentiation; haematopoietic stem cell; tyrosine; bone marrow; leukaemia.
                                                                                   295
                                                                                                            327
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                                                                                                                                                                  267
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                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                        30 LEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQG
                                                                                                                                                                                                                                                                                                                                                             ຫ
                                                                                                                                                                                                                                                                                                    DRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEGLD
                                                                                EMPPOSPANIYYKV 308
                                                                                                          DGPPQSPPNIYYKV
                                                                                                                                      LSISTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQ
                                                                                                                                                               GSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPYYIVQ 326
                                                                                                                                                                                           STDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLLKYRRRHRKHSPQHTTT
                                                                                                                                                                                                                     PTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP 266
                                                                                                                                                                                                                                                 NOEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTNGRSSTTSPFVKPNPGS 181
                                                                                                                                                                                                                                                                           SLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DRGAAHSLEPGKENLPGD 206
                                                                                                                                                                                                                                                                                                                       RRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE 149
                                                                                                                                                                                                                                                                                                                                                          LEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQA 61
                                                                                                                                                                                                                                                                                                                                                                                                                    132;
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 162-163; 193pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KASEI KOGYO KK
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94JP-0244433.
94JP-0262882.
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 619.5; DB 17;
Pred. No. 1.2e-42;
8; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17;
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standard;

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Query Match
Best Local Similarity
Matches 87; Conserv

Conservative

26.6%;

Score 492; DB 21; Pred. No. 7.5e-33; 1; Mismatches 1

Length 89

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Gaps

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Sequence

9

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The patent discloses a complex comprising of a B class ephrin and PDZ domain containing protein. B class ephrins function as ligands for Eph receptor tyrosine kinases (RTK) and possess a transmembrane element and a highly conserved cytoplasmic tail at the C-terminus, that contains a PDZ binding site. This complex is used in methods to modulate the interaction of a B class ephrin and PDZ domain containing protein and to identify modulator compounds. It is also used for modulating cellular processes like, axonogenesis, nerve cell interactions and regeneration of nerve cells. The complex is also useful for treating proliferative or differentiative disorders associated with this protein complex. The present sequence is the human ephrin B C-terminal cytoplasmic domain, comprising conserved sequences reminiscent of known or predicted binding sites for PDZ domains. Ephrin B3 is also known as NIERK-2, EIK-13, EFL-6, ELF-3 and LERK-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDZ domain; B class ephrin; Eph receptor tyrosine kinase; RTK; modulator; cellular process; nerve cell interaction; regeneration of nerve cell; axonogenesis; antiproliferative, proliferative disorder; treatment; differentiative disorder; human; cytoplasmic domain.
                                                                                                                                                                                                                                       Example; Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                Isolated complex for treating proliferative or differentiative disorders comprises B class ephrin and PDZ domain containing p
                                                                                                                                                                                                                                                                                                             WPI; 2000-400038/34.
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production of homogenous forms of clustered ligands is broadly applicable to improve the affinity and/or increase the activity of a ligand as compared to the native form of the ligand. Ephrin fusion proteins have been constructed, which may be useful for treating neurological disorders. The ephrin fusion proteins are preferably capable of binding to Elk receptor and are especially Ef1-6 antagonists. The fusion proteins were constructed after it was demonstrated that similar improved activities could be achieved using Tie-2 receptor ligands. Angiopoletin-1 (Ang-1) is a Tie-2 receptor ligand and is an agonist for Tie-2, whereas angiopoletin-2 (Ang-2) is a naturally occuring antagonist of the Tie-2 receptor. The fibrinogen domains (FD) of Ang-1 and Ang-2 are the receptor-binding domains and dimerized versions, of e.g. Ang-1-FD-Fc
                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide encoding a fusion polypeptide, useful for promoting differential function and influencing phenotype, comprises two subunits containing at least one copy of the receptor binding domain of a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA51346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davis
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/note= "Derived from ephrin-B2 ectodomain
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Best Local Similarity
Matches 111; Conserv
                                                                                                                                           Key
Peptide
                                                                                                                                                                                    Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Ang-1 fibrinogen domain fused to an Pc domain), can bind to the Tie-2 receptor with much higher affinity than monomeric Ang-1-FD (dimerization occurs between the Pc components of adjacent molecules). However, Ang-1-FD-FC is not able to induce phosphorylation (activate) the Tie-2 receptor on endothelial cells unless it is further clustered with goat anti-human Pc antibodies. The novel fusion proteins, mutant versions of Ang-1-FD and Ang-2-FD, were designed that were intrinsically more highly clustered. Tie-2 agonist fusion proteins may be used as haematopoietic factors. Tie-2 receptor antagonist fusion proteins may be used disorders of blood forming organs, e.g. thrombocythemias, polycythemias
                                                                                                                                                                                                                            Ephrin-B1;
Efl-6 anta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Region
                        Peptide
                                                                           Peptide
                                                                                                                                                                                                                                                                   Ephrin-B1-Ephrin-B1-FC fusion protein.
                                                                                                                                                                                                                                                                                              26-SEP-2000
                                                                                                                                                                                                                                                                                                                         AAY96781;
                                                                                                                                                                                                                                                                                                                                                 AAY96781 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and leukemias.
                                                   Protein
                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                    428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V---DSKTVGQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARPPGPHSSPNYEFYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                    PKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                               P-----PFCPHYEKVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAAD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ASSAGSARNHGPTRRPELE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAG
                                                                                                                                                                                                                           n-B1; ELK receptor; ligand; dimer; Fc
antagonist; neurological.
                                                                                                                                                                                                   1
                                                                                                                                                                                   Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.5%;
ilarity 34.6%;
Conservative 32
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSSTTSPFVKPNPGSSTDGNSAGHSGNNLL
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                                                                                                                    /label= Signal_peptide
/note= "derived from E
                                      /label=
                                                              'label = Bridging_peptide
                                                                                         /label= ELK-L_ectodomain_1
                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LLGGPGIV----LEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPK 265
                                                                                                                                                                                                                         neurological.
                                                                                                                                                                                                                                                                                                                                                 Protein;
                           . 451
                                                    .448
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           Bridging_peptide
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Pred. No. 1.2e-28;
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                                                                                                                    ELK-L
                                                                                                                      Ectodomain
                                                                                                                                                                                                                                            domain;
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RESULT 26
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                                                                                                                                                                                                                                                                                                                      CC production of homogenous forms of clustered ligands is broadly applicable CC to improve the affinity and/or increase the activity of a ligand as CC compared to the native form of the ligand. Ephrin fusion proteins have been constructed, which may be useful for treating neurological CC disorders. The ephrin fusion proteins are preferably capable of binding CC to Elk receptor and are especially Ef1-6 antagonists. The fusion proteins are proteins are preferably capable of binding CC to Elk receptor and are especially Ef1-6 antagonists. The fusion proteins CC Angiopoietin-1 (Ang-1) is a Tie-2 receptor ligands. Angiopoietin-1 (Ang-1) is a Tie-2 receptor ligand and is an agonist for CC fie-2, whereas angiopoietin-2 (Ang-2) is a naturally occuring antagonist CC of the Tie-2 receptor. The fibringen domains and dimerized versions, of e.g. Ang-1-FD-FC (Ang-1 fibringen domain fused to an FC domain), can bind to the Tie-2 receptor with much higher affinity than monomeric Ang-1-FD (dimerization cocurs between the FC components of adjacent molecules). However, CC Ang-1-FD-FC is not able to induce phosphorylation (activate) the Tie-2 receptor on endothelial cells unless it is further clustered with goat anti-human FC antibodies. The novel fusion proteins, mutant versions of CC Ang-1-FD and Ang-2-FD, were designed that were intrinsically more highly CC clustered. Tie-2 agonist fusion proteins may be used to CC diagnose or treat, e.g. myeloproliferative or other proliferative and listered for and lenkemias.
                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide encoding a fusion polypeptide, useful for promoting differential function and influencing phenotype, comprises two subunits containing at least one copy of the receptor binding domain of a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 12; Fig 14A-E; 97pp; English
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                                                                                                                                                                                                                                                                                                                                                 leukemias.
                                                                                                                                                         EQAAACSTVLDENVLVTCNRPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYITSTSNGSLE 354
                                                                                                                                                                                                            GKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP----YEYYKLYLVRP 294
                                                                                                                                                                                                                                       GLSLEPVYWNSANKREQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGG 86
                                                   DSDGKHETVNQEEKSGP-----GASGG
                                                                             DPTSNATSRGAEGPLPPPSMPAVAGAAGG
                                                                                                      GLENREGGVCRTRIMKIIMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQAPGSRGSLG 414
                                                                                                                               GLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE-PGKENLPG 205
                                                                                                                                                                                 AQGRRCEAPPAPNILLICORPOLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTRE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-442670/38
                                                                                                                                                                                                                                                                   l Similarity
92; Conser
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                                                                                                                                                                                                                                                                                                                      683
                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                        24.5%; bred. No. 1...
44.0%; Pred. No. 1...
14.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yancopoulos GD,
                                                                                                                                                                                                                                                                Score 452.5; DB 21;
Pred. No. 1.5e-28;
2; Mismatches 72;
                                                                            234
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to new isolated soluble polypeptides comprising an amino acid sequence of an extracellular region of an Eph B receptor or an amino acid sequence of an ephrin B ligand, or essentially similar amino acid sequence of extracellular region of an Eph B receptor or an amino acid sequence of an ephrin B ligand. Extracellular region of an Eph B receptor is capable of binding with high affinity to a mammalian ephrin B ligand. Ephrin B ligand is capable of binding with high affinity to a mammalian Eph B receptor. The nucleic acid encoding the polypeptides or the polypeptides are useful for producing pharmaceutical compositions for treating a tumour disease or ocular necvascularisation in mammals, including humans. The vector is useful in producing a pharmaceutical composition for treating the diseases cited above in mammals, particularly humans, by means of gene therapy. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New soluble polypeptides of the extracellular region of the Eph B receptor and ephrin B ligands, useful in gene therapy for treating a tumor disease or ocular neovascularization in mammals, including humans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 48-49; 55pp; English
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171
                                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                         74 PNYEFYKLYLVGGAQGRRCEAPPAPNILLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                      DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA
                                                                                                                                                                                                                            GOYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                                                                                                          GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                       HSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRR
                                                                                                           DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ephrin B2 ligand
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- ASSAGSARNHGPTRRPELE - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.2%; Score 447; DB 23; 36.4%; Pred. No. 1.1e-28; tive 33; Mismatches 80
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194
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RESULT 27
AAB244020
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AC AAE24

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New soluble polypeptides of the extracellular region of the Eph B receptor and ephrin B ligands, useful in gene therapy for treating a tumor disease or ocular neovascularization in mammals, including humans
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         134
                                                                                                                                                                                             14
                                                                                                                                                                                                                                                        14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYFQIGDRLDLLCFRARPPGPHSS
                                                                     71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVA
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         DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
                                                                                                                                                                                             GVIMVICRTAISKSIVIEPIYWNSSNSKFIPGQGLVIYPQIGDKIDIICPKV----DSKTV 70
                                                                     GOYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                          PNYEFYKLYLVGGAQGRRÇEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Page 51-52; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ephrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVARTIS AG. NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               229 AA;
                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                 23.9%; Score 443; DB 23; 35.6%; Pred. No. 2.4e-28; tive 36; Mismatches 79;
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AAWO6333
ID AAWO66333
ID AAWO66333
ID AAWO66333
ID AAWO663X
XX AAWO6
XX 119an
XX Recep
XW Recep
XW Homo
XX JP081
XX JP081
XX JP081
XX WP17
XX AAWO6
CC AAWO6
CC Incore
CC Teprer
CC Teprer
CC Proce
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1994;
19-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor-type tyrosine kinase; ligand; coomassie staining; PAS staining;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ligand #1 for receptor-type tyrosine kinase protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New ligand for receptor type tyrosine kinase - has mol.wt. 22
kilo:dalton(s) and is positive for Coomassie and PAS staining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-388601/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-ЛИТ-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192
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DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQ-----
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NQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTNGRSSTTSPFVKPNPGS
                                            SLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DRGAAHSLEPGKENLPGD
                                                                                                                                         RRCEAPPAPNILLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE
                                                                                                                                                                                                                   RRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREA
                                                                                                        1 Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 43; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                195 AA;
                                                                                                                                                                                                                                                                                                                                     Conservative
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94JP-0253848.
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                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                  Score 431.5; DB 17;
Pred. No. 1.7e-27;
2; Mismatches 66;
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RESULT 29
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor-type tyrosine kinase; LPM medium; ligand; autophosphorylation; insect cell; animal cell; growth promoter; undifferentiated cell; insulin; interleukin; fibroblast growth factor; hepatocyte growth factor; nerve growth factor; interferon-gamma; tumour necrosis factor; inducer.
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPM cell culture medium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-014848/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW11307 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 38-39; 45pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                       interleukin, a fibroblast growth factor, or interferon-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor-type tyrosine kinase ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ASAH ) ASAHI KASEI KOGYO KK
182
                              207
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                                                               122
                                                                                            150
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                                                                                                                                                           90
                                                                                                                                                                                                                         30 LEPVYWNSANKREQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQG 89
                                                                                                                                                                                          σ
                                                                                                                           DRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEGLD
ST-DGNSAGHSG 192
                                PTSNATSRGAEG 218
                                                                                            SLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DRGAAHSLEPGKENLPGD 206
                                                                                                                                                           RRCEAPPAPULLITCURPDIDIRFTIKFQEYSPULWGHEFRSHHDYYIIATSDGTREGLE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ST-DGNSAGHSG 192
                                                               NQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTNGRSSTTSPFVKPNPGS
                                                                                                                                                                                          LEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQA
                                                                                                                                                                                                                                                         l Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                        195 AA;
                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                     45.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for culturing
                                                                                                                                                                                                                                                         Score 431.5; DB 18;
Pred. No. 1.7e-27;
2; Mismatches 66;
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RESULT 30
AAM37671
ID AAM37671
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AC AAM37
XX Pepti
XX Pepti
XX Probe
KW Probe
KW Genet
XX WO200
XX O4-FI
PR 26-MI
PR 30-JI
PR 30-JI
PR 30-JI
PR 30-JI
PR 27-SI
PR 27-SI
PR 27-SI
PR 27-SI
PR 27-SI
PR 10-XI
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP: see ARI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
Human; single exon probe; asthma; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
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                                           Human peptide encoded by genome-derived single exon probe
                                                                                                                                                                                             ABG46524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID No 37940; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-CCT-2001
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                                                                                                                                                                                                                                                                                                                                                            102 LTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYI 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                VTCNRPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYI
                                                                                                                                                                                                                                                                                                                                                                                                            FLSGKGLVIYPKIGDKLDIICPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 52; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
                                                                                                                                                                                          standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0608408.
2000US-0632366.
2000US-0234687.
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2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0207456
                                                                                              (first entry
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Pred. No. 7.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
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Mismatches 24;
  cancer; COPD; ILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
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Connicies acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of complements or the 12387 open reading frames derived from the 12614 probes, also included are a microarray comprising the novel set of probes, the novel set of probes which hybridise at high stringency to a collection acid expressed in the human lung; measuring gene expression in a connucleic acid expressed in the human lung; measuring gene expression in a connucleic acid expressed in the human lung; measuring gene expression in a connucleic acid expressed in the human lung; measuring gene expression in a collection of detectably labeled nucleic acids derived from human lung measuring at least one exon from genome, comprising the label detectably bound to each probe of the entaryote; and (b) detecting specific hybridisation of detectably cof the entaryote; and (b) detecting specific hybridisation of detectably cof the entaryote; and (b) detecting specific hybridisation of detectably conspirating (a) identifying exons from genomic sequences of the entaryote; and (b) detecting specific hybridisation of detectably comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons in factor of the exons in several to the exons should be assigned to a single exon pattern of expression of the exons in the tributable to the exons in serial pattern of the exons should be assigned to a single exon pattern of the exons in a gene, particularly the expression of the exons 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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; 2000US-236359P.
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2000US-207456P.
2000US-0608408.
2000US-0632366.
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n human lung
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patent

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230 GAAGGLA--

-LLLLGVAGAGGA-----

--MCWRRRRAKPSESRHPGP

266

Query Match Best Local : Matches

similarity

11.1%; 37.7%;

Score 205.5; Pred. No. 3.

5e-09;

Indels

Gaps

5

DB

22;

Length

136; 39;

Conservative

13;

Mismatches

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30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                         The present invention relates to single exon nucleic acid probes see AAI31315-AAI57546). The present sequence is a peptide encode such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples from human placenta. The probes are useful for antenatal diagnos human capacita.
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                                                                                                                                                                                                                                                                                                                                                                                    Probe; microarray;
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #11571 encoded by probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM37534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM37534 standard;
Sequence
                  human genetic disorders.
                                                                                           Claim 27; SEQ ID No 37803; 654pp;
                                                                                                              analyzing
                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                  SG
                                                                                                              genome-derived single exon nucleic acid zing gene expression in human placenta -
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52; Conservative
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2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-0234687.
2000US-0234685.
2000US-0236359.
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 1814 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung; measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detectably specific hybridisation of detectably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary clitary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human peptide encoded by genome-derived single
                                                                                                                                                                                                                                                                                                          Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-114183/15
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                                                                                                                                                                                                                                                                          27; SEQ ID No 36059; 634pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC.
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2000US-207456P.
2000US-0608408.
; 2000US-0632368.
; 2000US-234687P.
2000US-236359P.
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CC Note: The sequence data for this patent did not form particularion.
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                       pDZ domain; B class ephrin; Eph receptor tyrosine kinase; RTK; modulator; cellular process; nerve cell interaction; regeneration of nerve cell; axonogenesis; antiproliferative; proliferative disorder; treatment; differentiative disorder; human; cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                 Human ephrin B2 C-terminal cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                    04-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                       AAY71437 standard; peptide; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                 Modified-site
                                                                  Modified-site
                                                                                                    Modified-site
                                                                                                                                       Region
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52; Conser
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                                                                                                                                    Location/Qualifiers
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71..75
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              "Conserved
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                                                                                 "Conserved tyrosine
                                                                                                                     "Conserved region"
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Pred. No. 3.5e-09;
.3; Mismatches 34;
              tyrosine phosphorylation site"
                                                tyrosine
                                                  phosphorylation
                                                                                     phosphorylation
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XX AB54
XX U9-M2
XX Humar
XX Humar
XX Humar
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XX Active
XW Active

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 41
Human, pancreas, pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated complex for disorders comprises E
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                                                                                                                   Human pancreatic cancer antigen protein sequence
                                                                                                                                                                      09-MAR-2001
                                                                                                                                                                                                                       AAB54187;
                                                                                                                                                                                                                                                                     AAB54187 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                      (first entry)
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Pred. No. 2.5e-09;
4; Mismatches 11
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                                                                                                                        SEQ ID
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                                                                          AAY71436;
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(first entry)

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consists and antigen pancreatic disorders, especially cancer condition parcellar and antipolic and susceptive, and can be used to detect, treat or prevent pancreatic disorders, especially cancer at the activities and can be used for conditions or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the condition or a susceptibility to one in a subject. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be used for. The concertic cancer antigens can be used to design nucleic canceric cancer antigen polynucleotides can be used to design nucleic candalysis, tissue identification and/or typing and a variety of forensic cand diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to generate antibodies contains can be used to generate antibodies can be used to generate antibodies. The proteins can be used to generate antibodies can be used to treat to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AkC99232 to Ak29240 and AkB5467 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 1078; 1379pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences used in the exemplification of the present invention.
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                                                                      291 GELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                        235 LALLILIGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGL----GGGGGMGPREAEP 290
                                                                                                                                                             LTVLLLKL----
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                                                                                                                                                                                                                                                                                                                           Conservative
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-TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV 106
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                                                                                                                                                             ·RKRHRKHTQQ------RAAALSLSTLASPKGGSGTAGTEP
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Pred. No. 4.5e
|1; Mismatches
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Human

ephrin

B1 C-terminal cytoplasmic domain.

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308 CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV

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                                                                                                                                                  The patent discloses a complex comprising of a B class ephrin and PDZ domain containing protein. B class ephrins function as ligands for Eph receptor tyrosine kinases (RTK) and possess a transmembrane element and a highly conserved cytoplasmic tail at the C-terminus, that contains a PDZ binding site. This complex is used in methods to modulate the interaction of a B class ephrin and PDZ domain containing protein and to identify modulator compounds. It is also used for modulating cellular processes like, axonogenesis, nerve cell interactions and regeneration of nerve cells. The complex is also useful for treating proliferative or differentiative disorders associated with this protein complex. The present sequence is the human ephrin B1 C-terminal cytoplasmic domain, comprising conserved sequences reminiscent of known or predicted binding sites for PDZ domains. Ephrin B1 is also known as LERX-2, Elk-L, PDZ domains. Ephrin B1 is also known as LERX-2, Elk-L, PDZ domains.
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                                                                                                               Sequence
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                                                                                                               82 AA;
                                                        Conservative
                                                                                                                                           and STRA1.
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                                                                    10.9%;
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                                                       Score 201; DB 21;
Pred. No. 4.4e-09;
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Matches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITS-ABLIGIT), expressed DNA sequences (ABLIGITS) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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11-JUL-2000;
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  KENLPGDPTSNATSRGAEG-----
                                                  KDDLYRRIGGRCSTNN/KVVFKVCCAPEDNN-KTTALSNSKSVTDTGGAINVNIANNDES
                                                                                                                                                          KVEYETCRITNADPRVIAICDKPQKLMFFTITFRPFTPQPGGLEFLPGNDYYFISTS--S
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DB; ABL02724.
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Pred. No. 1.9e-06;
0; Mismatches 136;
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                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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genes from Drosophila and
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11-JUL-2000; 2000US-0614150
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33 VYWNSANKRFQAEG-GYVLYPQIG---
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                                                                        9.8%; Score 182; DB 22; llarity 22.9%; Pred. No. 1.9e-06; Conservative 50; Mismatches 136;
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04-APR-1994;
12-APR-1994;
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       Ligands which bind Eph neurological disorders
                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                       neurological
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                                                                                                                                                           04-APR-1995;
                                                                                                                                                                               12-OCT-1995.
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Yancopoulos
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                                    1995-358635/46.
DB; AAT03883.
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                                                                                            REGENERON PHARM
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                                                                                                                                                                                                                                                                                                                         L; Eph transmembrane tyrosine kinase family
disorder; identification; diagnosis.
                                                                        Davis S,
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                                                                                                             94US-0327423.
94US-0222075.
94US-0229402.
94US-0299567.
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218..235
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                  family receptors
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Best Local S
Matches 64
                                                                                                                                                                                                              30-AUG-1993;
03-DEC-1993;
09-MAY-1994;
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                              WPI; 1995-106811/14.
N-PSDB; AAQ85887.
                                                                                                                                                                                                                                                                                                                                              17-AUG-1994;
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Conservative 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                          Cerretti
                                                                                                                                                                                                           93US-0109745.
93US-0114426.
93US-0161132.
94US-0240124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                            94WO-US09282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ν
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; dd85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine kinase receptor; tumorigenesis;
                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 181; DB 16;
Pred. No. 6.7e-07;
3; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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RESULT 41
AAW02587
ID AAW02
XX AAW02
XX 28-NO
DE Lerk-
XX Lerk-
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XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFFXSXOCOCOCOCOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis) It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of detecting hek or hek-L in invitro assays, and to carry diagnostic or
                                                         WPI; 1996-287171/29.
N-PSDB; AAT32700.
                                                                                                                                                                                                                                                           01-MAR-1995;
06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW02587 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hek proteins, to purify hek proteins, and to carry diagnostic of cytotoxic agents to particular leukaemia cells that express the antigen. Hek-L also binds the elk tyrosine kinase receptors.
                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lerk-7; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lerk-6; hek; elk; cell surface receptor; culture; reagent;
neuron; disorder; injury; delivery agent; diagnostic; ther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lerk-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW02587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated DNA encoding hek-L protein or its fusion products useful as assay reagent or for carrying therapeutic and diagnostic compounds to leukaemia cells.
                                                                                                                                                                                                                                                                                                                                            05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9617925-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 21; Page 36; 45pp; English.
                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 RKPVSEMP-----PGKENLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 also AAR71482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVÇLTRGMKVLLRVGQSPRGGAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPG-----GALG----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                           95US-0396946.
94US-0351025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine.
                                                                                                                                                                                                                                                                                                                                            95WO-US15781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 179; DB 1
Pred. No. le-06;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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12;

isolated human Lerk-7 cytokine -

which binds

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cell surface

FEXSKORORORORORA

7;

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ARESULT 42
AAR91283
ID AAR91
XX AAR91
XX 10-OC
XX 10-CC
XX 1ERK-
XW 1ERK-
XW 10-OC
XX MUS m
XX W0961
XX 03-OC
PR 03-OC
PR 03-OC
PR 05-OC
XX WPI;
DR WPI;
DR WPI;
DR WPI;
DR WPSI
XX 1B-Ol:
PT 1sol:
PT SCTel
XX SCTel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a murine cytokine, Lerk-6, encoded by ART32700. A fragment of murine Lerk-6 DNA was isolated by PCR for use a probe for a human Lerk-6 homologue. The probe however led to the identification of a human Lerk-7 gene (see ART32699). The Lerk-7 gene and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for delivering diagnostic or therapeutic agents to cells, e.g. cancer cells. The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic properties and can be used to treat neural tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 35; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptors elk, hek for treating neural
                                Isolated DNA encoding cytokine designated LERK-6 which binds to and elk cell surface receptors - useful for drug delivery and
                                                                                                                                                                                                     03-OCT-1995;
05-OCT-1994;
                                                                                                                                                                                                                                                        04-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                       LERK-6; hek; elk; cell surface receptors; culture; reagent;
neurons; disorder; injury; delivery agent; diagnostic; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR91283 standard;
                screening procedures
                                                                                    N-PSDB;
                                                                                                                                     Cerretti
                                                                                                                                                                                                                                                                                        18-APR-1996
                                                                                                                                                                                                                                                                                                                        WO9610911-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            LERK-6 protein
                                                                                                                                                                     AWWI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150
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                                                                                    1996-209575/21.
DB; AAT14009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYWNSANKRFQAE----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAPEPIFTSNSSCSGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDP----TSNATSRGAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                       IMMUNEX
                                                                                                                                     ₽P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PNLVDRPCLR - -LKVYVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.5%;
ilarity 29.3%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                    95US-0538709.
94US-0318393.
                                                                                                                                                                                                                                                        95WO-US12779
                                                                                                                                                                       CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and eck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 176; DB 17;
Pred. No. 1.3e-06;
9; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for delivering agents to cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTNETLY 149
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The LERK-6 polypeptide encoded can be used to isolate cells expressing hek/elk cell surface receptors, or to measure the biological activity of such receptors. The protein may also be used as a delivery agent, taking diagnostic and therapeutic agents to cells expressing such receptors. LERK-6 can also be used as a tissue culture reagent to enhance the viability or prolong the lifespan of the neurons. Neural tissue disorders and injuries may be treated by
                                                                                                                                                                                                                                                                                                                                                                LERK-6 polypeptide; hek receptor; elk receptor; human; murine; cell proliferation; neural growth; neural tissue; neurological neurodegenerative; excitotoxicity.
The invention relates murine and human LERK-6 polypeptides that bind hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombing production of the proteins. LERK-6 polypeptides may be useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                           WPI; 1999-243567/20.
N-PSDB; AAX32761.
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                                                                                                                                                                      Cerretti DP;
                                                                                                                                                                                                                                                                                  04-MAR-1999.
                                                                                                                                                                                                                                                                                                           WO9910495-A1
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                                                                       Claim
                                                                                                New cytokine designated LERK-6
                                                                                                                                                                                                  ( VMMI)
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                                                                                                                                                                                                                                                       27-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE
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                                                                       <u>σ</u>,
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58; Conservative
                                                                                                                                                                                               IMMUNEX
                                                                     Page 37-38;
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                                                                     46pp; English.
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Pred. No. 1.3e-06;
9; Mismatches 69
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disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enhancement, stimulation, prolifthek or elk receptor. The ligand neural growth, development and/o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
  19-SEP-1995;
                                                        28-MAR-1996.
                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse EPH receptor ligand Elf-1
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                                                                                                           WO9609384-A1
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     95WO-US11869
                                                                                                                                                                                                                                                                                                                                                 /label=
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Pred. No. 1.3e
19; Mismatches
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L.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis and treatment of disorders associated with the Elf-1 gene, e.g.
   Modified-site
                                Protein
                                                                                                      Mus sp.
                                                                                                                                                 Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase liga:
B61; LERK-2; proliferation; differentiation; intracellular signalling;
increased; survival; neuronal cell; neuron survival; treatment;
Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilag
                                                                                                                                                                                                                             Amino acid sequence of a mammalian Elf-1 protein.
                                                                                                                                                                                                                                                           20-0CT-1998
                                                                                                                                                                                                                                                                                        AAW71006;
                                                                                                                                                                                                                                                                                                                     AAW71006 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 86; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheng H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-1995;
19-SEP-1994;
                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dementia, tachycardia , etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                                                                                                          152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYWNSANKREQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA
                                                                                                                                     formation.
                                                                                                                                                                                                                                                                                                                                                                                             EAPEPIFTSNSSCSGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                           GDP----TSNATSRGAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1996-188446/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Similarity 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT15008
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNLVDRPCLR - - LKVYVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flanagan JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.5%;
ilarity 29.3%;
Conservative 1
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94US-0308814.
 /note= "mature protein"
38
                           /note= "signal peptide"
21...209
                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                          218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 176; DB 17;
Pred. No. 1.5e-06;
9; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTNETLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                     cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Best Local S
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19-SEP-1994;
27-FEB-1995;
                                                                                                                                                                                                                                                                                                                   The present sequence represents a mammalian RPH receptor ligand designated Blf-1. This ligand can bind to both mek-4 and sek-AP. Blf-1 a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other BPH receptor ligands, B61 and LRRK-2. The Blf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended framsplantation), also therapeutically in increase neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding Elf-1 protein that binds to EPH-type - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                            hepatocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARD ) HARVARD COLLEGE.
                                                   152
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5
                                                                                                                                                                                     33 VYWNSANKRFOAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
EAPEPIFTSNSSCSGLGG
                                                                                                                                                            VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE
                         GDP----TSNATSRGAEG 218
                                                   ----PNLVDRPCLR--LKVYVR-
                                                                             REGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP
                                                                                                       GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP--
                                                                                                                               CGRECEVED PROTECT --- DIE LIKE OS SENT MCHELE SHHDALITALS DCL
                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV42926
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flanagan JG;
                                                                                                                                                                                                                                                                     209 AA;
                                                                                                                                                                                                                                                                                                            to form an artificial liver,
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2A; 53pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0455001.
94US-0308814.
95US-0393462.
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                                                                                                                                                                                                                             9.5%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "contains core sequence motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "contains a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "potential N-linked glycosylation site"
                                                                                                                                                                                                               19;
                                                                                                                                                                                                                             Score 176; DB 19;
Pred. No. 1.5e-06;
                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-linked glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-linked
                                                                                                                                                                                                                                                                                                            to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycosylation
                                                                                                                                                                                                                  69;
                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                            209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           site'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
                                                                                                                                                                                                               Gaps
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RESULT 46 AAY06822

09-MAR-2001

(first entry)

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AAB54058
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                                                                                                                                                                                                                                                                                                                                                       The invention relates murine and human LERK-6 polypeptides that bind to chek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant comprising the LERK-6 nucleic acid sequences are used for the recombinant components of the proteins. LERK-6 polypeptides may be useful in the component of the proteins. LERK-6 polypeptides may be useful in the component of the proteins of the proteins of the proteins of the complex may be involved in computating growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological compurodegenerative conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the elk or hek cell surface receptor. The present sequence represents a trophic conducting the conducting collappetide.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-243567/20
N-PSDB; AAX32767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06822 standard; Protein; 213
                                                             AAB54058 standard;
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 42; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cytokine designated LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP
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                                  AAB54058
                                                                                                                                          98
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                                                                                                                                          GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFOLFTPFSLGFEFRPGHEYYYISAT
                                                                                                                                                                                                                                  VYWNSANKREOA----EGGYVLYFOIGDRLDLLCFRARFEGFHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                        QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                                                                                                       VYMNRSNPRPHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE
                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US17772
                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry
                                                                                                                                                                                                                                                                  9.5%; Score 175.5; DB 20
36.8%; Pred. No. 1.7e-06;
tive 14; Mismatches 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  injury;
disease;
                                                                                                                                               154
                                                                                                                                                                                                                                                                       Gaps
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AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to CC AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used concerning, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a concerning can be identified. The proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to graventing antieris to the antigens can be used to garcies can be identified. The pancreatic cancer antigens can be used to garcreatic cancer antigens can be used to design nucleic candists and antagonists to the antigens can be used to design nucleic candispositic methods. The proteins can be used to generate antibodies can define the used to purify detect and target the polypeptides, including continue and in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to generate antibodies can definite antibodies can defin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAC98823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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120 YSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSFRGGAVFRK 179
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                                                                                                                                YE---DHSVADAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQR 123
                                                                                                                                                                                                                   ARPPGPHSSPN--YEFYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQE 119
                                                                                                                                                                                                                                                                                                                                                                                        PGGVRVGALLILGVIGIVSGLSL---EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR 64
                                                                                                                                                                                                                                                                                                          PGQARAMEFLWAPLIGICCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pancreas; pancreatic cancer; pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 172.5;
Pred. No. 3.1e
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 3.1e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218;
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EEPLP--AERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLKFSEKFQLFTP

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ARESULT 48
AAR94767
ID AAR94
XX AAR94
XX D2-JU
XX Chick
XX Elf-1
XX diagn
XX Gallu
XX Gallu
XX Key
FT Prote
FT Regic
FT 
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                                                                                                                                                           Query Match
Best Local S
Matches 49
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diagnosis;
                                                                                                                                                                                                                                                                                                           A novel chicken EPH receptor ligand, Elf-1 (AAR94767), is involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It is the product of a cDNA clone (AATLS009) obtd. from an embryo cDNA expression library. This cDNA is used for the produ. of recombinant Elf-1, which can be used to modulate proliferation, survival and/or differentiation of cells and tissues, and to stimulate or antagonise intracellular signal transduction pathways mediated by the EPH-type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine and chicken EPH receptor ligand, {\tt Elf-1} - useful in diagnosis and treatment of disorders associated with the {\tt Elf-1} gene, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR94767 standard; Protein; 200 AA
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 88-89; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dementia, tachycardia , etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-1995;
19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9609384-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 FTPFTLGKEFKEGHSYYYISKPIHQHEDR-----CLRLKVTVSGKITHSPQAHDNPQE 176
                                                                                                           15
                                                                                                                                                                                          Local Similarity
                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1996-188446/19.
RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSP 122
                                                  AALLAAIVG-VCVWSDDPGKVISDRYAVYWNRSNPRFH-RGDYTVEVSINDYLDIYCPHY 64
                                                                                                           ALLLLGVLGLVSGLSLEP------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ
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                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT15009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor ligand; dementia; tachycardia; transgenic animal.
                                                                                                                                                                                                                                                                      200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor ligand Elf-1.
                                                                                                                                                                Conservative
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94US-0308814.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=
33..157
/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Mat_protein
                                                                                                                                                                                       35.3%;
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                                                                                                                                                                16;
                                                                                                                                                                                          Score 172; DB 1
Pred. No. 3e-06;
                                                                                                                                                                Mismatches
                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                   Length 200;
                                                                                                                                                                   Indels
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123

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RESULT 49
AAW71007
Query Match
Best Local S
Matches 49
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19-SEP-1994;
27-FEB-1995;
                                                                                              The present sequence represents an avian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-Rp. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositel linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended for transplantation), also therapseutically in increase neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61, LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-CCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW71007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW71007 standard; Protein; 200
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV42927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5795734-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     artificial liver; cartilage; bone formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino
                                                                                                                                                                                                                                                                                                 Claim 1; Columns 75-78; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Cheng H,
                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                      1998-466665/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid
l Similarity
49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 Flanagan JG;
                                                         200
 Conservative
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94US-0308814.
95US-0393462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 61..150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35..157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "contains a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "contains a Cys4"
             35.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an avian
   16;
                Score 172; DB 1
Pred. No. 3e-06;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elf-1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      core sequence
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                            19;
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                              Length 200;
    Indels
      16;
      Gaps
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Query Match Best Local Matches

66;

Conservative

Similarity

9.24;

Score 169.5; DB 1 Pred. No. 4.9e-06; 8; Mismatches 82

82; 16;

Indels Length

Gaps

10;

201; 55,

Sequence

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RESULT 50
AAR71482
ID AAR71
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                                                                                                                                                                                                                                                                                                     20-AUG-1993;
30-AUG-1993;
03-DEC-1993;
09-MAY-1994;
                              The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek antign. Hek-L also binds the elk tyrosine kinase receptors.
                                                                                                                                                                       New isolated DNA encoding hek-L protein or its fusion useful as assay reagent or for carrying therapeutic andiagnostic compounds to leukaemia cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human hek-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR71482;
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                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                       Beckmann MP,
                                                                                                                                                                                                                                                                                                                                                               17-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ligand; cell
                                                                                                                                                                                                                                                                                                                                                                                                           WO9506065-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogen.
                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP.
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                        also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLLIGVIGLYSGISLEP-------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEPLP--AERMERYVLYMVNYEGHASCDHROKGFKRWECNRPDSPSGPLKFSEKFQLFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AALLAAIVG-VCVWSDDPGKVISDRYAVYWNRSNPRFH-RGDYTVEVSINDYLDIYCPHY
                                                                                                                                                                                                                                  1995-106811/14.
                                                                                                                                                   21; Page 38; 45pp; English.
                                                                                                                                                                                                                       AAQ85888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                        AAR71481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            surface;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                         Cerretti
                                                                                                                                                                                                                                                                                                     93US-0109745.
93US-0114426.
93US-0161132.
94US-0240124.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "signal peptide"
23..201
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine kinase receptor; tumorigenesis;
                                                                                                                                                                                                                                                         DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141
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                                                                                                                                                                                       on products and
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ļ. !	165	202	137	142	77	83	20	24
	165GSPGESGTSGWRGGDTPSPLCLLLL 189	202 NLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240	137TPESSGQCL 164	142 DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKE 201	WVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTFFSLGFEFLFGETYYYISVP 136	83 LVGGAQGRRCEAP-PAPNILLITCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141	LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALY 76	24 LVSGLSL-EPVYMNSANKRPQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82

Search completed: February 11, 2003, 12:03:00 Job time : 32.2264 secs

Title: Perfect score:

Scoring table:

Minimum DB Maximum DB

3

protein

1

sequence

2 Appli 3 Appli 3 Appli 4 Appli 6 Appli 6 Appli 7 Appli 8 Appli 8 Appli 8 Appli 8 Appli 9 Appl

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Post-processing: Minimum Match 0%
Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/POTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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    262574 seqs, 29422922 residues
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-436-044-2
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US-08-488-077-2
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US-08-488-077-2
US-08-488-077-2
US-08-29-567-68-2
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Retent No. 6413730

GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
APPLICANT: Mosmalu, Geraldine
APPLICANT: MUSUNION: OLIGOMERIZED RECEPTORS WHICH APPLICATION: BY TRANSMEMBRANE LIGANDS FOR ELK
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/09/214, 631
CURRENT APPLICATION NUMBER: PCT/CA97/00473
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
INUMBER OF SEO ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 340
TYPE: PRT
CRGANISM: Homo sapiens
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US-09-214-631-3
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Best Local Similarity
Matches 339; Conserv
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                                            VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                           SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMXVLLQVGQSPRGGAVPRKP
                                                                                                                     SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
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nilarity 99.7%;
Conservative
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US-09-165-533-2
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US-08-455-001-2
PCT-US95-158-01-2
US-08-308-814-2
PCT-US95-11869-2
US-09-173-492-10
US-09-173-492-10
US-09-173-133-10
US-09-173-133-10
US-09-173-133-10
US-09-173-134-4
US-08-455-001-4
PCT-US95-11869-4
US-08-453-124-4
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US-09-134-631-8
US-09-214-631-8
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Pred. No. 1.1e-146;
1; Mismatches 0;
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AFFECT PATHWAYS REGULATED ELK-RELATED RECEPTOR

Length 340; Indels

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Gaps

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240 180 120 60

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Result No.

Score

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US-08-436-044-2
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Best Local Similarity
Matches 139; Conserv
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GENERAL INFORMATI
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                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION UNWBER: 00,000
REFERENCE/DOCKET NUMBER: 902D
TELECONMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/252-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genencech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bennett, Brian D. APPLICANT: Matthews, William TITLE OF INVENTION: HTK LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                   14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/436,044 FILING DATE: 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                GLLMVLCRTAISRSIVLEDIYMNSSNSKFLDGQGLVLYPQIGDKLDIICPKV---DSKTV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG
                                 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLLGVAGAGGAMC 250
                                                                                             DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                             GOYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                               PNYEFYKLYLVGGAQGRRCEAPPAPNILLITCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
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GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 25:
                                                                    DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGFTRRPELEAGTN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94080
                                                                                                                                                                                                                                                                                                                                                                                                    f: 336 amino acids amino acid
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                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-1994
                                                                                                                                                                                                                                                                                       34.5%; Score 637.5; DB 1;
42.1%; Pred. No. 1e-45;
Live 49; Mismatches 129;
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US-08-436-054-2
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 336 amin -
Type
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Patent No. 5864020
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Matthews, William
TITLE OF INVENTION: HTK LIGAND
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 139; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy
COMPUTER: ISM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277722
FILING DATE: 20-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254
                                   194
                                                                                                        134
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 251
                                                                191 GAAHSLEPGKENLPGDETSNATSRGAEGELPPPSMPAVAGAAGGLALLLLLGVAGAGGAMC
                                                                                                                                        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05
CLASSIFICATION:
                                                                                                                                                                            74 GOVEYYKVIMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                17 GLÍMVÍCKTAISKSIVÍÉÞIÝMNSSNSKFLÞGQGLVÍLÝÞQÍGÐKÍÐIICÞKV---DSKTV 73
                                                                                                                                                                                                                                                                     14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGFHSS 73
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: am.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                          PNYEFYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WRRERAKPSESRHPGPGSFGRGGSLGLGGGGGGGGGREAEPGELGIALRGGGAADPPFCPH 310
                                   GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR----TADSVFCPH
 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGRGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                        DYYIISTSNGSLEGIDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGFTRRPELEAGTN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Genentech, Inc.
T: 460 Point San Bruno
South San Francisco
: California
                                                                                                                                                                                                                                                                                                                                                                                                                            amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                      34.5%; Score 637.5; DB 2;
42.1%; Pred. No. 1e-45;
tive 49; Mismatches 129;
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                                       253
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RESULT 4
PCT-US95-08812-2
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                           Query Match 34.5
Best Local Similarity 42.1
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 902P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311
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                                                                        194
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
TOPOLOGY: line-
                                                                                                            191
                                                                                                                                                                                                                  74
                                                                                                                                                                                                                                                                                        17
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                                                                                                                                                                                                                                                                                                                       14 GALLLIGVIGIVSGISLEPVYWNSANKRFQAEGGYVLYPQIGDRIDLICPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
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KYRRHRKHSPOHTTILSISTLATPKRÖGNN----NGSEPSDVIIPIR---TÄDSVFÖPH
                                    WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                    GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                        DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                                                                                  GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                                                      GLIMVICRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
                                                                      GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253
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42.1%; Pred. No. 1e-45;
rative 49; Mismatches 129;
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RESULT 5
US-08-213-403-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5512457
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
TOPOLOGY: line
WOLFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION MOMBER: US/08/213,403
FILING DATE: 15-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                 179
                                                                                                  182
                                                                                                                                   119
                                                                                                                                                                  122
232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ----
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STATE: Washington
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                                                                                                                                                                                                   64 CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98101
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                                                                                                                                                                                                                                                                                                     PGGVRVGALILLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                  PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                                                                                                                                                                                     CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                           SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP--
                                                                                                  SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
                                                                                                                                                                                                                                                                        PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII
                                                                                                                                   PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08213403
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                             Indels 58;
                                                                     -GASGGSSGDPD 231
 ----RAAALSL
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; MOLECULE TYPE: protein
US-08-458-077-2
                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                            Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
PILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/
PILING DATE: 13-NOV-1992
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R
APPLICANT: Baum, Peter R
APPLICANT: Carpenter, Melissa
TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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     119
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ZIF: 98101
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                                                                                                                                                                        8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                               PNIWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                   CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANIYYKV 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
     PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                                                                                                                         PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
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5627267
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                                                                                                                                                                                                                                                                                                                          amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 University Street
                                                                                                                                                                                                          34.2%; Score 632; DB 1
ilarity 39.5%; Pred. No. 3e-45;
Conservative 48; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunex Corporation
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-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version 5.1a
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                                                                                                                                             i LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-741-2
                                                                                                                                                                                                                                                                                                                                                                                  CLANTING SYSTEM: Apple System 7.1
SOTTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,741
FILING DATE: 02-UN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
CLASSIFICATION: 530
CLASSIFICATION: 530
ATTORNEY/AGENT TYPESSO
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Patent No. 5670625
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R
                                                                      Matches
                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-6644
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acid
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Carpenter, Me
TITLE OF INVENTION: NO.
NUMBER OF SEQUENCES: 2
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                               8 PGGVRVGALĻLLGVLGLVSGL-----SLEPVXWNSANKRFQAEGGVVLYPQIGDRLDLL 61
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PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
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                                                                    Score 632; DB 1; Length 346; Pred. No. 3e-45; B; Mismatches 116; Indels
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, MOLECULE TYPE: protein US-08-747-240-2
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US-08-747-240-2
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                                                                                                                                                                                               CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807-A
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 587-0430
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APPLICANT: Lyman,
APPLICANT: Beckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,240
FILING DATE: 12-NOV-1996
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PELICANY: Baum, Peter R
PELICANY: Baum, Peter R
PELICANY: Carpenter, Melissa
PELICANY: Carpenter, Melis
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                                                                              TOPOLOGY:
                                                                                                                 LENGTH: 346 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
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Beckmann, M. Pati
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                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: 32,143
REFERENCE/DOCKET NUMBER: 37,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08299567
Patent No. 5747033
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Best Local Similarity 39.5
Matches 145; Conservative
                                                                                                                                                                     TELEFAX: 914-345-7721 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH PAMILY LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 ANIYYKV 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 -----LLLLGVAGAGGA------MCWRRRAKPSESRHPGPGSFGRGGSLGL
                          STRANDEDNESS:
TOPOLOGY: ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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STATE: New York
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                                                                                  amino acid
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777 Old Saw Mill River Road
                                                                                                                                                                                                   914-345-77
protein
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RESULT 10
US-08-436-044-4
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Best Local Similarity
                                                                                                                   APPLICATION NUMBER: US/08/436,044
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277722
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REGISTRATION NUMBER: 00,000
REGISTRATION NUMBER: 902D3
               TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                   ZIP: 94000
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
SEQUENCE
                                                                                       REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Genented, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bennett, Brian D. APPLICANT: Matthews, William TITLE OF INVENTION: HTK LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340
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                                   TELEPHONE: 910/-
TELEPHONE: 910/-
TERRAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANIYYKV 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LLLLGVAGAGGA-------MCWRRRRAKPSESRHPGPGSFGRGGSLGL
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 CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                     415/225-1994
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                                                                                                             902D3
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Pred. No. 3e-45;
8; Mismatches 116; Indels
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US-08-436-054-4
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Query Match
Best Local Similarity
Matches 135; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GALLLIGVLGIVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 GVIMVICRTAISKSIVLEÞIYMNSSNSKFLÞGQGLVLYÞQÍGDKLDIICÞKV---DSKTV 70
YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                            YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                 KYRRRHRKHSPOHTTTLSLSTLATPKRSGNN----NGSEPSDIIPLR---TADSVFCPH 303
                                                                                                                                                                    WRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                                                                                             GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250
                                                                                                                                                                                                                                                                                GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                                                                                                                                                                                        DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDFTRRPELEAGTN 190
                                                                                                                                                                                                                                                                                                                                                                                           DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.0%; Score 629.5; DB 1;
40.9%; Pred. No. 4.6e-45;
tive 52; Mismatches 130;
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Geneatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,054
FILING DATE: 05-MX-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWNER: 08/277722
FILING DATE: 20-UTL-1994
ATTORNEY/AGENT INFORMATION:
NAME: 1-0- Wendy M. Sequence 4, Application US/08436054 Patent No. 5864020 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEPAX: 415/952-9881 APPLICANT: Bennett, Brian D. APPLICANT: Matthews, William TITLE OF INVENTION: HTK LIGAND CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: STATE: COUNTRY: STREET: 460 Point San Bruno CITY: South San Francisco ADDRESSEE: INFORM California USA amino acids 902D1 Blvd

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US-08-271-948-2
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Patent No. 6303769
GENERAL INFORMATION:
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Best Local (
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                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION UNMBER: 32,172
REFERENCE/DOCKET NUMBER: 2823
TELEPHONE: (206) 587-0430
TELEPHAX: (206) 233-0644
                                                                                           TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,948
SEQUENCE CHARACTERISTICS:
LENGTH: 3.3 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cerretti, Douglas P.
APPLICANT: Reddy, Pranhitha
TITLE OF INVENTION: No. 6303769el Cytokine Designated Lerk-5
NUMBER OF SEQUENCES: 3
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CLASSIFICATION:
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GY: linear
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51 University Street
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40.9%; Pred. No. 4.6e-45;
tive 52; Mismatches 130;
                                                                                              2:
                                                                                                                                                                                        2823
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PCT-US95-08534-2
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                 TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
TOPOLOGY: linear
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GENERAL INFORMATION:
APPLICANT: Immunex Corporation
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                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,948
FILING DATE: 08-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2823-WO
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08534
FILING DATE: 06-JUL-1995
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CORRESPONDENCE ADDRESS:
ADDRESSES: Immunex Corporation
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TITLE OF INVENTION: Novel Cytokine Designated Lerk-5
MOLECULE TYPE: protein
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CITY: Seattle
STATE: Washington
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PCT-US95-08812-4
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                                                       ; TOPOLOGY: PCT-US95-08812-4
                                                                                TELEPHONE: 415/225-1994
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
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Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application GENERAL INFORMATION:
APPLICANT: Generation
Query Match
Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08
                                                                                                                                                                 NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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  Conservative
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 34.0%; Score 629.5; DB 5;
40.9%; Pred. No. 4.6e-45;
tive 52; Mismatches 130;
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                                                                                                                                                                                                                                                                                                                                                                                                360 Kb floppy disk
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  Indels
                          Length 333;
  13;
  Gaps
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US-09-214-631-4
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     WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
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251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                         191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                                                                                                                                                                                      GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIFFVIIITLVVLLL
                                                                                                                                                                                                                                                                                DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
                                                                                                                                                                                                                                                                                                                                                                                 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                      YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                       DYYIISTSNGSLEGIDNQEGGVCQTRAMKIIMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
                                                                                                                            310
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CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
NUMBER: OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 333
TYPE: PRT Sequence 4, Application US/09214631 Patent No. 6413730 GENERAL INFORMATION: Query Match 33.6%; Score 622.5; DB 4; Best Local Similarity 40.9%; Pred. No. 1.8e-44; Matches 135; Conservative 54; Mismatches 128; APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
APPLICANT: Pawson, Tony
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR
TITLE OF INVENTION: TYROSINE KIMASES
FILE REFERENCE: 11757, 23USWO 14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ-SPRGGAVPRKPVSEMP-MER-DR 190 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250 DYYIISTSNGSLEGIDNQEGGVCQTRAMKIIMKVGQDASSAGSTPNKDPTRRPELEAGTN 190 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSFNLWGLEFQKNK 130 PNYEFYKLYLVGGAQGRRCEAPPAPNILLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133 GVLMVLCRTAISKSIVLEÞIYMNSSNSKFLÞGQGLVLYÞQIGDKLDIICÞKV---DSKTV 70 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250 AFFECT PATHWAYS REGULATED ELK-RELATED RECEPTOR Indels Length 333; 13; Gaps 9

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RESULT 17
US-09-214-631-13
US-09-214-631-13
Esquence 13, Application US/09214631
Patent No. 6413730
GENERAL INFORMATION:
APPLICANT: Holland, Sacha
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US-09-214-631-5
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-631-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application Patent No. 6413730 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.9%; Score 608.5; DB 4; Best Local Similarity 38.7%; Pred. No. 2.7e-43; Matches 142; Conservative 50; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
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                                                                                                                                         339 ANIYYKV 345
                                                                                                                                                                                                                                                                         232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLFKRHRKHTQ------RAAALSL 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 KYRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVPCPH
                                                                                                                                                                         334 PNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 CPPÁEAGRP-----YÉYYKLYLVRPEÓAAAĆSTVLDPMVLVTCNRPEQEIRFTIKFQEFS 118
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                                                                                                                                                                                                           STIASPKGGSGTAGTEPSDIIIPL---FTTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 338
                                                                                                                                                                                                                                                                                                             -----LILLGVAGAGGA------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                                                                                                                                                                                                                                                                                                                                             SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
                                                                                                                                                                                                                                                                                                                                                                               SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGGRWLGKWLYAMVVWALCRLATPLAKKLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGGVRVG----ALLLLGVLGLVSGL--SLEPVYWNSANKREQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                                                                                                                                                                                                                                                                                                                                                                                                PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                                                                                                                                                                                                                          ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
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CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 11
SEQ ID NO 11
LENGTH: 82
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                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Homo sapiens US-09-214-631-11
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US-09-214-631-11
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; ORGANISM: Homo sapiens
US-09-214-631-13
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SEQ ID NO 13
LENGTH: 89
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                             Matches
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Holland, Sacha
APPLICANT: Moamalu, Geraldine
APPLICANT: Moamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSIUE KINASES
FILE REFERENCE: 11757.23USWO
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APPLICANT: PAWSON, TONY
ITTLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
TILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
NUMBER: OF SEQ ID NOS: 13
NUMBER: OF SEQ ID NOS: 13
                                        308
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                                                                                                                           252 RRRRAKPSESRHPGPGSFGRGGSLGL----GGGGGMGPREAEPGELGIALRGGGAADPPF 307
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                                                                                                                                                                                                Local Similarity
                            CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                   RKRHRKHTQQ
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                                                                                                                                                                           44;
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ilarity 47.3%;
Conservative
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                                                                                   RAAALSISTLASPKGGSGTAGTEPSDIIIPLR---TTENNY 49
                                                                                                                                                                      Score 201; DB 4;
Pred. No. 5.1e-10;
9; Mismatches 24;
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82
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RESULT 19

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GENERAL INFORMATION:
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SEQ ID NO 12
LENGTH: 82
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                                                                                                                                                                                                                                                                                                   ZIP: 10591-6707

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
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CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mbamalu, Geraldine APPLICANT: Pawson, Tony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR TITLE OF INVENTION: TYROSINE KINASES FILE REFERENCE: 11757.23USWO
                                                                              TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 AEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 SEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tarrytown
New York
                                                              i: 234 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08299567
  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09214631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Regeneron Pharmaceuticals, Inc 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sacha
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Pred. No. 5.6
                                                                                                                                                                                                                      290
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ELK-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08240124 Patent No. 5516658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acid
                                                                                                                                                                                                                                                                                       FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                       NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER; 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 PTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                                                TELEFAX: 156822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: IMMUNEX CORPORATION STREET: 51 UNIVERSITY STREET CITY: SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 SSGAGÞGÞGGGGAEQÝVLÝMVSRNGYRTCNÁSQGFK-RWECNRÞHAÞHSÞIKFSEKFQRÝS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 28.4 es 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                  TOPOLOGY:
                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFSLGYEFHAGHSYYYISTPTHNLH------WKCLR--MKVFVCCASTSHSG---EKPV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98101
                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WASHINGTON
                                                        238 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CERRETTI,
                                                                                                                                   (206) 587-0430
(206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GALG-----NRHAVYWNŚSNOHLRRÉ-GYTVQVNVNDYĹDIYCPHYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOKINE THAT BINDS THE CELL SURFACE RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOUGLAS P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.7%; Score 179; DB 1;
28.4%; Pred. No. 1.3e-07;
ive 22; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/240,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 234;
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US-08-453-943-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local (
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                                                                                               INFORMATION FOR SEQ ID NO:
                                      SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
                                                                                                                                  NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/114,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETII, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 RKPVSEMP-----PGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: 1
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRYSAFSLGYEFHAGHEYYYISTPTHNLH--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPG-----GALG----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WASHINGTON
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                                                                                                                                                                                                                                                                                                                               30-AUG-1993
protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 179; DB 1;
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----WKCLR--MKVFVCCASTSHSG--- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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Patent No. 596911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 65; Conserv
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                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                      SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 RKPVSEMP-----
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                                                                                                 1EC-1000 (200) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLE OF INVENTION:
    COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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175 EKPVPTLPQFTMGENVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223
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                                                                                                                                                                                                                                                                                                                                                                       7 GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R 64
                                                                                                         QRYSAFSLGYEFHAGHEYYYISTPTHNLH------WKCLR--MKVFVCCASTSHSG--- 174
                                                                                                                                        QEYSPNIWGHEFRSHHDYYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGAVP 177
                                                                                                                                                                                                             SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                    -----GALG----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.7%;
                                                    ---MERDRGAAHSLE----PGKENLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 179; DB 1;
Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 238;
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                                                    204
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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APPLICATION NUMBER: US 08/161,132
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
PILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
PILING DATE: 30-AUG-1993
PRIOR APPLICATION INFORMATION:
APPLICATION INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/057,121 Application US/09057121 51 UNIVERSITY STREET , DOUGLAS P.
CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK 08/240,124

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US-09-358-734-2
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Best Local Similarity 28.4
Matches 65; Conservative
                                                                                                                            FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORWATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                              INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SCFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/114,426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/358,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPG-----GALG----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67
                                  : 238 amino acids
amino acid
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  TYPE:
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ZENTION: CYTOKINE THAT BINDS THE CELL SURFACE
ZENTION: RECEPTOR HEK
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protein
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; Pred. No. 1.3e-07;
24; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
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                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-299-567-7
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Best Local
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Best Local :
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                                                                                                               Matches
                                                                                                                                                                                                                                                                           TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: RE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/01
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: STREET: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 EKPVPTLPOFTMGPNVKINVLEDFEGENPOVPKLEKSISGTSPKREHLP 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                      33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--RARPPGPHSSPNYEFYKLYLVGGAQGR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
                                                                                                           Match 9.5%; Score 176.5; DB 1;
Local Similarity 31.9%; Pred. No. 1.1e-07;
les 43; Conservative 14; Mismatches 73;
                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                     VXWNSSNPKFXRXEGYTIXVXXNDYLDIICPHYEXXXXXXXAGXXXXECYXLYLVXXEXYX 60
RCEAPPAPULLLTCDRP---DLDLRFTIKFQEYSPULWGHEFRSHHDYYIIATSDGTREG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 28.4%;
65; Conservative
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                                                                                                                                                                                                                                                              amino acid
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777 Old Saw Mill River Road
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Pred. No. 1.3e-07;
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                                                                                                                                                Length 135;
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RESULT 27
US-08-920-440B-2
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US-09-609-324A-2
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APPLICANT: Cerret
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TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
FILE REFERENCE: A7772
CURRENT APPLICATION NUMBER: US/09/609,324A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 08/920,440
PRIOR PILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
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NUMBER OF SEQ ID NOS: 10
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PRIOR FILING DATE: 1995-10-03
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ORGANISM: LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 184
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
                                                                                                                                                                                                                          MINDER OF INVENTION: Cytokine De
                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                150 EAPEPIFTSNSSCSGLGG 167
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                                                                                    COUNTRY: USA
ZIP: 98101
                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 VYWNSANKRFQAE----GGYVLYPQIGDRLDLLCPRARPFGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PNLVDRPCLR--LKVYVR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFOLFTPFSLGFEFRPGHEYYYISATP-- 126
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                                                                                                                                                             51 University Street
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                          Immunex Corporation
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US-08-920-440B-2
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Best Local Similarity
Matches 58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440
FILING DATE: 29-AUG-1997
ATTONNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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APPLICATION NUMBER: US/08/920,440B
FILLING DATE: 29-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                              COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 51 Un
CITY: Seattle
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51 University Street
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TELEFAX: (206) 233-0644 INFORMATION FOR SEQ ID NO:

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Query Match
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Patent No. 6232447
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                                                                                                                                      TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO:
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LENGTH: 184 amino acids
                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CETTELLANT: CETTETTI, Douglas P.
RITLE OF INVENTION: Cytokine Designated LERK-6
UNDER OF SEQUENCES: 10
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                                                                                                                                                                                                                       NAME: Henry, Janis C. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYTIATSDGT 144
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les 58; Conservative
                                                                      TOPOLOGY:
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                                                                                                       LENGTH:
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                                                    TYPE: protein
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Best Local S
Matches 58
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Patent No. 6268482
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/538,709
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
OPERATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                              NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,658
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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les 58; Conserv
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GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFOLFTPFSLGFEFRPGHEYYYISATP--
                                  QGRRCEAPPAPNLLITCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
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                                                                   VYMNRSNPRPOVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 68
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51 University Street
                                                                                                                                  9.5%; Score 176; DB 4; Length 184; ilarity 29.3%; Pred. No. 1.7e-07; Conservative 19; Mismatches 69; Indels
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Cytokine Designated as LERK-6
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9; Mismatches 69
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RESULT 32
PCT-US95-15781-2
; Sequence 2, Application PC/TUS9515781
; GENERAL INFORMATION:
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PCT-US95-12779-2
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GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Patentin Release #1.0, Veri
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12779
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2826-WO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             145
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                                                                                                                                                                                                                                                                                                                                                                                                         'Match 9.5%; Score 176; DB 5; Length 184; Local Similarity 29.3%; Pred. No. 1.7e-07; ses 58; Conservative 19; Mismatches 69; Indels
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CITY: Seattle
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51 University Street
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In Release #1.0, Version #1.25
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; Sequence 2, Application US/08455001
; Patent No. 5795734
; GENERAL INFORMATION:
; APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
; TITLE OF INVENTION: EPH Receptor Ligands, an
; TITLE OF INVENTION: Thereto
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      RESULT 33
US-08-455-001-2
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Patentin Release #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/1
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/351,025
FILING DATE: 06-DEC-1994
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TITLE OF INVENTION: Cytokine Designated Lerk-7
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 0.
FILING DATE: 01-MAR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 126
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2829-WO
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CITY: Seattle
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51 University Street
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                                                                         Uses Related
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US-08-308-814-2
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFTOATTON: 000
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        Sequence 2, Application of the No. 6268476 GENERAL INFORMATION:
       ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CP2
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                 APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands,
TITLE OF INVENTION: Thereto
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ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                     175 EAPEPIFTSNSSCSGLGG 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                       COUNTRY: USA
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SOFTWARE:
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ASCII (txt)
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207-8941
227-2941
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29.3%; Pred. No. 2e-07;
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PCT-US95-11869-2
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                                                   MOLECULE TYPE: protein PCT-US95-11869-2
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Best Local Similarity 29.3%;
Matches 58; Conservative 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Applicati
GENERAL INFORMATION:
Query Match
Best Local Similarity
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                                                                                                                                                                                 TELEFAX: (617) 227-59
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: EPH Receptor Litifie OF INVENTION: Thereto NUMBER OF SEQUENCES: 5 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                  REGISTRATION NÜMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acid
                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 19-SEP-1994
                                                                                                 LENGTH: 209 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 QGRRCEAPPAPNILLICORPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93
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                                                                                                                                                                                                                                                                                                      Vincent, Matthew P.
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  9.5%;
29.3%;
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Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMI-011
  Score 176; DB 5;
Pred. No. 2e-07;
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                     Length 209;
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US-08-920-440B-10; Sequence 10, Application US/08920440B; Patent No. 5919905; Patent No. 5919905; GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 10
LENGTH: 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/538,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CERRETTI, Douglas P.
TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
FILE REFERENCE: A7772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1995-10-03
PRIOR APPLICATION NUMBER: 08/318,393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/609,324A
CURRENT FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: LERK-6
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                 NUMBER OF SEQUENCES: 1
                                                                                                                                                                                      APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 EAPEPIFTSNSSCSGLGG 192
                                                                           STREET: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 VYWNSANKRFQA-----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                          COUNTRY:
                                                                                                                               DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYWNSANKRFQAE----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
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7:
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                                                                                                                51 University Street
                                                          USA
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                                                                                                                                   Immunex Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%; Score 175.5;
36.8%; Pred. No. 2.3e
tive 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5; DB 1;
2.3e-07;
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RESULT 38
US-09-173-492-10
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TELEFAX: (206, 10 NO: 10 INFORMATION FOR SEQ ID NO: 10 SEQUENCE CHARACTERISTICS:
**NOTH: 213 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 567-0430
TELEPAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440B
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09173492 Patent No. 6194172
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Best Local
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                                                                           NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
APPLICATION NUMBER: US/08/
PILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
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OPERATING SYSTEM: System 7.6
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 VYWNSANKRFQA-----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 51 Uni
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51 University Street
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%; Pred. No. 2.3e-07;
14; Mismatches 51
                                                            10:
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US-09-173-133-10
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Patent No. 6232447
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                    TELEPAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                    NAME: Henry, Janis C.
REGISTRATION NUMBER: 24,347
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFOLFTPFSLGFEFRPGHEYYYISAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 VYWNSANKRFQA-----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
mes 43; Conserv
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 86
                                     88
                                                                      3
                                                                                                         33 VYWNSANKRFOA----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                            Match 9.5%;
Local Similarity 36.8%;
les 43; Conservative 1:
                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/173,133 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                          VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seattle
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51 University Street
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36.8%; Pred. No. 2.3e-07;
htive 14; Mismatches 51
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                                                                                                                                            ; Score 175.5; DB 4; ; Pred. No. 2.3e-07; 14; Mismatches 51;
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                                                                                                                                                                             Length 213;
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RESULT 40

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; TYPE: PRT; ORGANISM: Homo sapiens US-09-214-631-7
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LENGTH: 233
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CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSIUS KINASES
FILE REFERENCE: 11757.23USWO
                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
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APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
    ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
: MA
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INFORMATION:
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Vincent,

Matthew P

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PCT-US95-11869-4
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                                                                                                                                                                       Matches
                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: EPH Receptor Li
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                           TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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REFERENCE/DOCKET NUMBER: HMI-011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
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  65
                                                                                                                          15 ALLLIGVIGIVSGISLEP------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA 65
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TELEFAX: (617) 227-5941
                                      66 RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSP 122
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  EEPLP--AERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLKFSEKFQLFTP 122
                                                                                   AALLAAIVG-VCVWSDDPGKVISDRYAVYWNRSNPRFH-RGDYTVEVSINDYLDIYCPHY 64
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                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                         9.3%; Score 172; DB 5; Length 200; 35.3%; Pred. No. 4.1e-07;
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                                                                                                                                                                     16; Mismatches
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                                                                                                                                                                       58
7
                                                                                                                                                                       Indels
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Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08240124 Patent No. 5516658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/109,745
APPLICATION UNMER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE KATHRYN A.
                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CERRETTI,
                                 142 DGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKE 201
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                                                                                                                                                                                      24 LVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                             LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                           MVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVP 136
                                                                                                                                                    LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76
                                                                                                                                                                                                                                                                                                                                                                    amino acid
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CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
                                                                                                                                                                                                                                                   9.2%; Score 169.5; DB 1;
29.9%; Pred. No. 6.7e-07;
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-RLQVSVCCKERKSESAHPV---- 164
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US-08-453-943-4
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                                                                                                                                                                                                   Query Match
                                                                                                                                                                        Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
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137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
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                                                                                                                                         24 LVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSENYEFYKLY 82
                                                                                                                                                                                    Local Similarity
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 --TPE--
                        DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKE 201
                                                       WIDWPGYESCOAEGPRAYKRWYCSLPFGHYQFSEKIQRFTPFSLGFEFLFGETYYYISVP 136
                                                                                 LVGGAQGRRCEAP-PAPNILITCDRPDIDIRFTIKFQEYSPNIWGHEFRSHHDYYIIATS 14:
                                                                                                               LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76
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                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                        201 amino acids
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                                                                                                                                                                                    9.2%;
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                                                                                                                                                                                      Score 169.5; DB 1;
Pred. No. 6.7e-07;
                                                                                                                                                                         Mismatches
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 - RLOVSVCCKERKSESAHPV-----
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FILING DATE:
O3-DEC-1993
FRIOR APPLICATION NUMBER: US 08/161,132
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057 177
FILING DATE:
CLASCOTTON
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Patent No. 5969110
                                                                                                                                                                                 Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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APPLICANT: CERRETTI, DOUGI
142 DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKÞVSEMÞMERDRGAAHSLEÞGKE 201
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                                                                                                                                                24 LVSGLSL-EPVYMNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                  MVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEELPGETYYYISVP 136
                                                                                 LVGGAQGRRCEAP-PAPNILLITCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                  LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76
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                                                                                                                                                                                                                                                                                               amino acid
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51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                201 amino acids
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                  linear
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CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
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Pred. No. 6.7e-07
8; Mismatches 8:
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US-09-358-734-4
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Matches
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Patent NO. 6274117
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
APPLICANT: CYTOKINE THAT
TITLE OF INVENTION: RECEPTOR HEK
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 233-064-
TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
 137
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                            142 DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMFMERDRGAAHSLEFGKE 201
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                                                                                             83
                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                        24 LVSGLSL-EPVYMNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82
                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                             LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                           LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76
                                                            MVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVP 136
                                                                                                                                                                                        ch 9.2%;
l Similarity 29.9%;
66; Conservative 1
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: WASHINGTON
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                                                                                                                                                                                        Score 169.5; DB 4;
Pred. No. 6.7e-07;
8; Mismatches 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version
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   RLQVSVCCKERKSESAHPV---- 164
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                                                                                                                                                                                                                        Length 201;
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                                                                                                                                                                                          Indels 55;
                                                                                                                                                                                          Gaps
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APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
APPLICANT: Masmalu, Geraldine
APPLICANT: Masmalu, Geraldine
APPLICANT: Masmalu, Geraldine
APPLICANT: Masmalu, Geraldine
APPLICATION: TONY
TITLE OF INVENTION: DETANSMEMERANE LIGANDS FOR ELI
TITLE OF INVENTION: TROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER FILING DATE: 1996-07-05
NUMBER: OF SEQ ID NOS: 13
COLUMNER OF SEQ ID NOS: 13
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APPLICANT: Mamalu, Geraldine
APPLICANT: MITTON: OLIGOMERIZED RECEPTORS WHICH AFF
TITLE OF INVENTION: DIGOMERIZED RECEPTORS WHICH AFF
TITLE OF INVENTION: TROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
RARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
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US-09-214-631-8
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09214631
Patent No. 6413730
GENERAL INFORMATION:
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SEQ ID NO 8
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SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 LILGVL-----GLVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKSESAHPV-----GSPGESGTSGWRGGDTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPPEGP--ETFALYMVDWPGYESCQAEGPRGYKRWVCSLPFGHVQFSEKIQRFTPFSLGF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDRGAAHSLEPGKENLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVFRKFVSEMFME 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPHSSPNYETYKLYLVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGH 127
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ilarity 29.8%;
Conservative 1
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Pred. No. 7.4e-07;
9; Mismatches 84; Indels
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RESULT 49
US-08-442-248-4
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                                                                                                                                                   Query Match
Best Local S
Matches 65
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LENGTH: 209
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Patent No. 5759863
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                    TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27-OCT-1994
ATTORNBY/AGENT INFORMATION:
NAME: TOUCHIA, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-8674
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
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les 42; Conserv
                                                                                                                                                                                                                                                TYPE: amin
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/442,248 FILING DATE: 15-MAY-1995
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CITY: South San Francisco
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                                                                                                             33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG-----
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                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                            VYWNSSNERFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC 90
      DHTSKGFKRWECNRPHSPN---
                                    ----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
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                                                                                                                                                   h 9.1%; Score 167.5; DB 1; Similarity 28.8%; Pred. No. 1.2e-06; 65; Conservative 29; Mismatches 81;
                                                                                                                                                                                                                                                                  amino acid
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35.9%; Pred. No. 8.5e-07;
ative 14; Mismatches 52
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  --GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS 141
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RESULT 50
US-08-440-815-4
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,815
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOrchia, Timothy E.
REGISTRATION NUMBER: 36,700
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acid
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MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
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                                  198
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187
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                                                                                                                                         91 DHTSKGFKRWECNRPHSPN------GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS
                                                                                                                                                                            86
                                                                                                                                                                                                               34 VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC 90
                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C1
                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE 197
                                PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA 243
                                                                                                      S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE 197
                                                                                                                                                              -----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA 243
                                                                     AIPDNGRRS-----
PADDTV---HESAEPSRG-ENAAQTPRIPSRL--
                                                                                                                                                                                                                                                                                        65;
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Similarity 28.8%; Pred. No. 1.2e-06;
65; Conservative 29; Mismatches 81
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 -LAILLFLLA 223
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                                                                                                                                                                                                                                                                                                                           Length 228;
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Search completed: February 11, 2003, 12:06:26 Job time : 14.6918 secs

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Maximum
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1850
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(c) 1993 - 2003 Compugen Ltd.
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JERK-7 precursor -
B61 protein precur
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collagen alpha 3 (I
collagen alpha 3 (I
collagen alpha 3 (I
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ephrin-A2 - human
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Stral/Eplg2 protei
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LERK-4 - human
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ALIGNMENTS

RESULT

hepatoma transmembrane kinase ligand - mouse
C;Species: Mus musculus (house mouse)
C;Ate: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 05-Nov-1999
C;Accession: 149766
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthew Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EMP-related receptor protein-tyrosine ki. A;Reference number: 149766; MUID:95199254; PMID:7534404
A;Recession: 149766
A;Status; preliminary; translated from GB/EMBL/DDBJ
A;Molecular type: mRNA
A;Recession: 1-336 <RES>
A;Reference number: 1-336 <RES>
A;Reference mRNA
A;Residues: 1-336 <RES> Ś 밁 Ś 밁 Ś 밁 Ś 밁 A;Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678 C;Genetics: Ś よ S A; Gene: HTK Query Match 34.5%; Score 637.5; DB 2; Best Local Similarity 42.1%; Pred. No. 1.9e-37; Matches 139; Conservative 49; Mismatches 129; 311 194 191 134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190 74 17 74 YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340 WRRRAKESESRHEGEGSEGRGGSLGLGGGGGGGGGEREAEFGELGIALRGGGAADEFFCEH GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH Indels 13; Length Gaps 310 253 73 5

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hepatcma transmembrane kinase ligand - human
(;Species: Homo sapiens (man)
;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: 184743
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin
A;Reference number: 149766; MUID:95199254; PMID:7534404
A;Accession: 184743
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-333 <RES-
A;Cross-references: GB:L38734; NID:9769675; PIDN:AAC41752.1; PID:9769676
C;Genetics:
A;Gene: GDB:EPIG5; LERK5
A;Cross-references: GDB:438338; OMIM:600527
A;Map position: 13q33-13q33
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A;Title: Molecular characterization of a family of ligands for eph-related tyrosine kins A;Reference number: S46993; MUID:94349923; PMID:8070404
A;Accession: S46993
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A; Residues: 1-346 <BEC>
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;Date: 15-Jul-1995 #sequence_revision
;Accession: S46993
Matches
                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ----
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135;
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                34.0%;
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  52
Score 629.5; DB 2;
Pred. No. 6.8e-37;
2; Mismatches 130;
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73 73

SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLICCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132

YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPHQEIRFTIKFQEFSPNYMGLEFKKY

72

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A:Status: preliminary; not compared with cor
A:Molecule type: mRNA
A:Residues: 1-89, T',91-345 <SHA>
A:Crose-references: GB:U12983; NID:g575928;
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 148780; A55507; A55062; S52670
R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, Dev. Biol. 170, 420-433, 1995
Bev. Biol. 170, 420-433, 1995
A;Reference number: 148780; MUID:95377533; PMID:7649373
                                                                                                                                                                                                                                            A;Cross-references: GB:U07598
R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.
J. Biol. Chem. 269, 26606-26609, 1994
A;Title: CDNA cloning and characterization of a ligand for the A;Reference number: A55062; MUID:95014510; PMID:7929389
A;Accession: A55062
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859
R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins,
Genomics 24, 127-13, 1994
A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene
A;Reference number: A55507; MUID:95203867; PMID:7896266
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                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-345 <FLE>
                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: A55507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-345 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: 148780
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                                                                                                                             A;Gene: EPLG2
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                                                                       Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGRGFREAEPGELGIALRGGGAADPPPPCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFÄGIÄSGCIIFIVIIITLVVLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYYIISTSNGSLEGLDNQEGGVCQTRAWKILMKVGQDASSAGSTRNKDPTRRPELEAGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
ALLLLGVIGLVSGL--SLEPVYMNSANKRFQAEGGYVLYPQIGDRLDLLCPRARFPGPHS
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                                                                       Similarity
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse
                                                                       33.2%;
                                                       51;
                                                   Score 613.5; DB 2;
Pred. No. 9.3e-36;
1; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB/EMBL/DDBJ
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                                                                                                                                                                                                                             conceptual
                                                                                                                                                                        PIDN:AAA53231.1; PID:g575929
                                                                                                                                                                                                                                 translation
                                                         Indels
                                                                                            Length
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                                                         Gaps
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R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollin Oncogene 9, 3241-3248, 1994
A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conser A;Reference number: I58406; MUID:95022634; PMID:7936648
A;Accession: I58406
A;Accession: I58406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 KRES
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RESULT 6
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Best Local Simi
Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                               189
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                                                      345 V 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                           HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ-----RAAALSLSTLASP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKT-----ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGGGGDSDSFFNSK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHSLEPGKENLPGDPTSNATSRGAEGP------LPPPSMPAVAGAAGG------LA
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                                                                                                                                                                                                                                     LLLIGVAGAGGA-----GG 279
                                                                                                                                                                                                                                                                               VKT-----ATQAPGRGSQGDSDGKHETVNQQEKSGPGAGGSGSGDTDSFFNSK 236
                                                                                                                                                                                                                                                                                                                AHSLEPGKENLPGDPTSNATSRGAEGP-----LPPPSMPAVAGAAGG------LA 236
                                                                                                                                                                                                                                                                                                                                                                                                                              ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPQQEIRFTIKFQEFSPNYMGLEFKKY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYK
                                                                                          V 340
                                                                                                                               KGDSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYK 344
                                                                                                                                                                 GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYK 339
                                                                                                                                                                                                      VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---
                                                                                                                                                                                                                                                                                                                                                       HDYYITSTSNGSLEGIENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 608.5; DB 2; Length ; Pred. No. 2.1e-35; 52; Mismatches 107; Indels
                                                                                                                                                                                                        RAAALSISTLASP 287
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A;Molecule type: DNA
A;Residues: 1-237 <WIL>
A;Coss-references: EMB1:Z82262; PIDN:CAB54195.1; GSPDB:GN00022; CESP:C43F9.8
A;Experimental source: clone C43F9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T19914
hypothetical protein C43F9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19914
R;Mortinore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19195
A;Accession: T19914
A;Atctus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-238 < RES>
A; Cross-references: EMBL:U14187; NID:g642832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change C;Accession: I3849
R;KOzlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Oncogene 10, 299-306, 1995
Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: A;Teference number: I3849; MUID:95140419; PMID:7838529
A;Accession: I38849
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C,Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                    A;Gene: GDB:EPLG3
A;Cross-references: GDB:438336; OMIM:601381
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A; Introns: 32/2; 96/3; 214/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                           65
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  68
                                                                                       24
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                                                                                       GPG-----GALG----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67
                                                                                                                            GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R
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SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF
                                         ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
                                                                                                                                                                               h 9.7%; Score 179; DB 2; I Similarity 28.4%; Pred. No. 1.4e-05; 65; Conservative 24; Mismatches 80;
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25.7%; Pred. No. 4.7e-08;
ative 41; Mismatches 83;
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ELF-1 protein precursor - mouse
N;Alternate names: Cek7 ligand
C;Species: Mus musculus (house mouse)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change
C;Accession: A54984; A55873
R;Cheng, H.J.; Flanagan, J.G.
Cell 79, 157-168, 1994
A;Title: Identification and cloning of ELF-1, a developmentally
A;Reference number: A54984; MUID:95007776; PMID:7522971
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                                                        Biochem. Biophys. Res. Commun. 252, 378-382, 1998
A;Title: Cloning, chromosal mapping, and tissue expression of
A;Reference number: JE0322; MUID:99045414; PMID:9826538
A;Accession: JE0322
A;Status: preliminary
                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence
C;Accession: JE0322
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A;Molecule type: mRNA
A;Residues: 1-209 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 270, 3467-3470, 1995
J.Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine
A;Reference number: A55873; MUID:95181289; PMID:7876076
A;Accession: A55873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <CHE>
                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-213 <AAS>
                                                                                                                                                                                                                                                      ephrin-A2 - human
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Matches 58
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                                                                                                                                                                                                                                                                                                                                                                                                          GDP----TSNATSRGAEG
                                                                                                                                                                                                                                                                                                                                                                 EAPEPIFTSNSSCSGLGG
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58; Conservat
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  GB:AJ007292;
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NID: g3688367;
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Pred. No. 2e-05;
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  PIDN:CAA07435.1;
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  PID:g3688368
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LERK-4 - human

C;Species: Homo sapiens (man)
C;Cate: 29-May-1998 #sequence_revision 29-May-1998 #text_change
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change
C;Accession: 138850
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.;
Cncogene 10, 299-306, 1995
Cncogene 10, 299-306, 1995
Cncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk:
A;Title: Ligands for the receptor tyrosine kinases hek and elk:
A;Title: Ligands for the receptor tyrosine kinases hek and elk:
A;Title: Ligands for the receptor tyrosine kinases hek and elk:
A;Title: Ligands for the receptor tyrosine kinases hek and elk:
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C.Species: Gallus gallus (chicken)
C.Date: 03-Nov-1995 #text_change 20-Jun-2000
C.Accession: A57084
R.Drescher, U.; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, M.; Bonhoeffer, Cell 82, 359-370, 1995
A.Title: In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa tectal paragraphs and the second paragraphs and the second paragraphs. A57084; MUID:95360980; PMID:7634326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAGAAGGLALLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMP--A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSEKFOLFTPFSLGFEFRPGREYFYISSAIPDNGRRS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTIKFQEYSPNLWGHEFRSHHDYYIIATS---DGTREGLESLQGGVCLTRGMKVLLRVGQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARPPGPHSSPNYEFYKLYLVG------GAQGRRCEAPPAPNLLLTCDRPDLDLR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PANSCMKTIGVHDRVFDVNDKVENSLEPADDTV---RESAEPSRG-ENAAQTPRIPIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                     #sequence_revision 29-May-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%; Score 170.5; DB 2; 28.9%; Pred. No. 5.3e-05; tive 30; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 175.5; DB 2
Pred. No. 2.2e-05;
4; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                  isolation of
                                                                                                                                                                                                                                                 Teepe, M.; Lyman,
                                                                                                                                                                                                                                                                                                            29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 φ.
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A;Cross-references:
C;Genetics:
A;Gene: GDB:EPLG4
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A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P.; Neuron 14, 973-981, 1995
A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved A;Reference number: I58170; MUID:95267434, PMID:7748564
A;Accession: I58170
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A;Cross-references: GDB:568757; OMIM:601535
A;Map position: 13q33-13q33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Status: preliminary, translated from GB/EMBL/DDBJA;Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-228 <KOZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:S77167; NID:g914184; PID:g914185
R;KOzlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, I
submitted to the EMBL Data Library, May 1995
A;Reference number: G08477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-228 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U26403; NID:g1019430; PIDN:AAB60377.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: G01812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: AL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LERK-7 precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)

Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999;

Accession: IS8170; G01812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBJ
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   142
                                                                       141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 NLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKE 201
                                                                                                                                           91
                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                      33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG------ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 MYDWPGYESCOAEGPRAYKRWYCSLPFGHYQFSEKIQRFTPFSLGFEFLPGETYYYISVP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
       AIPDNGRRS-
                                                                   S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE 197
                                                                                                                                              DHTSKGFKRWECNRPHSPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVGGAQGRRCEAP-PAPNLLITCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                                                                                                              ----GAQGRRCEAPPAPNILLITCDRPDLDLRFTIKFQBYSPNLWGHEFRSHHDYYIIAT 140
                                                                                                                                                                                                                                                                                      VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGINDYLDIVCPHYEGPGPPEGP--ETFALY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.2%; Score 169.5; DB 2
29.9%; Pred. No. 5.5e-05;
tive 18; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.1%;
       CLK--LKVFVR---
                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 167.5; DB 2;
; Pred. No. 8.7e-05;
29; Mismatches 81;
                                                                                                                                           -GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS 141
       - PTNSCMKTIGVHDRVFDVNDKVENSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RLQVSVCCKERKSESAHPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.P.; Carpenter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g1019431
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
       186
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                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-285,'A',287-680 <ELI>A;Residues: 1-285,'A',287-680 <ELI>A;Residues: 1-285,'A',287-680 <ELI>A;Cross-references: EMBL:X67348; NID:950480; PIDN:CAA47763.1; PID:950481
A;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen A;Reference number: S22215; MUID:92182017; PMID:1543751
A;Accession: S22215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.
MOL. Cell. Biol. 10, 5830-5838, 1990
A;Title: A novel immediate-early response gene of endothelium A;Reference number: A36377; MUID:91042512; PMID:2233719
A;Accession: A36377
A;Status: preliminary
A;Molecule type: mXNA
A;Residues: 375-450,'K', 452-627 <ELA>
A;Residues: 885-450,'K', 452-627 <ELA>
A;Cross-references: EMBL:X63013; NID:S
R;Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text change 13-Aug-1999 C;Accession: S31216; S288071; S32215; S30127; 148299; S26397; S31830 R;Kong, R,Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; (Eur. J. Blochem. 213, 99-111, 1993 Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; (April 1) Richem. 213, 99-111, 1993 Thomas, J.T.; Boot-Handford, R.P.; Grant, M.F.; (April 1) Richem. 213, 99-111, 1993 Thomas, J.T.; Boot-Handford, R.P.; Grant, M.F.; (April 1) Richem. 213, 99-111, 1993 Thomas, J.T.; Boot-Handford, R.P.; Grant, M.F.; (April 1) Richem. 213, 99-111, 1993 Thomas, J.T.; Boot-Handford, R.P.; Grant, M.F.; (April 1) Richem. 213, 99-111, 1993 Thomas, J.T.; Boot-Handford, R.P.; Grant, M.F.; (April 1) R.F.; (April 1) Richem. 213, 99-111, 1993 Thomas, J.T.; (April 1) Richem. 213, 99-111, 1993 Thomas, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collagen alpha 1(X) chain precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Sep-193 #sequence revision 30-Se C;Accession: S31216; S28807; S22215; S30127.
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A36377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z21610; NID:g49793; PIDN:CAA79736.1; PID:g49794 R;Elima, K.; Berola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Pera Biochem. J. 289, 247-253, 1993
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A;Residues: 1-205 <RDL>
A;Cross-references: GB:M57730; GB:M37476; NID:g179320; PIDN:AAA58388.1; PID:g179321
C;Superfamily: axon guidance signal protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and A;Reference number: S28807; MUID:93143676; PMID:8424763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-680 <KON>
A;Cross-references: EMBI
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;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                       NID:g49795;
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                                                                           PIDN: CAA44741.1;
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                                                                              PID: 949796
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: EMBL:X85121; MID:g50482; PIDN:CAA46237.1; PID:g667031
A;Cross-references: EMBL:X85121; MID:g50482; PIDN:CAA46237.1; PID:g667031
A;Cross-references: EMBL:X85121; MID:g50482; PIDN:CAA46237.1; PID:g667031
A;Cross-references: EMBL:X85121; MID:g50482; PIDN:CAA46237.1; PID:g667031
A;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibody
A;Reference number: S26397; MUID:88087150; PMID:2826450
A;Reference number: S26397; MUID:88087150; PMID:2826450
A;Residues: 'SDGYFSQ',24-26,'KQ' <SUM>
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Anap position: 10
A;Introns: 51/3
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
C;Keywords: colled coll; extracellular matrix; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted csIGo-
E:10-680/Dpc/Air. collagen alpha 1(VIII) Chain; complement Clq carboxyl-terminal homology
C;Keywords: colled coll; extracellular matrix; glycoprotein; homotrimer
collagen alpha 1(III) chain - bovine (Species: Bos primigenius taurus (cattle) (?Species: Bos primigenius taurus (cattle) (?Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 07-May-1999 (?Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946 R;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehr Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
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A;Residues: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L
R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
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Matches 97
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                                                                                                                                                                                                                                                                                                                 -GAPGPAGIATKGLNGPTGPP
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Pred. No. 0.0011;
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F;1-14/Region: amino-terminal nonhelical telopeptide
F;15-1040/Region: helical
F;557-589/Region: cell attachment (R-G-D) motif
F;557-574/Region: cell attachment (R-G-D) motif
F;875-877/Region: cell attachment (R-G-D) motif
F;878-880/Region: cell attachment (R-G-D) motif
F;878-880/Region: cell attachment (R-G-D) motif
F;935-937/Region: cell attachment (R-G-D) motif
F;1041-1049/Region: cell attachment (R-G-D) motif
F;1041-1049/Region: cell attachment (R-G-D) motif
F;107,119,938,950/Modified site: 5-hydroxylysine (Lys) #status expenience f;107,950/Modified site: allysine (Lys) (covalent) #status experimental
F;107/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;1040,1041/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are C;Comment: The type III collagen molecule is a trimer of identical chains, linked to ear C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology C;Keywords: colled coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol F;1-1049/Product: collagen alpha 1(III) chain #status experimental <CAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A38002; MUID:80026028; PMID:488908
A;Accession: A38002
A;Molecule type: protein
A;Residues: 423-571 <BEN>
R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
HOppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A;Reference number: A38003; MUID:80026029; PMID:488909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: S71946
A;Molecule type: protein
A;Residues: 87-106;1017-1029;1037-1049 <HEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 318, 497-503, 1996
A; Title: Cross-link analysis of the C-telopeptide domain
A; Reference number: S71946; MUID:96404897; PMID:8809038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A38005
A;Molecule type: protein
A;Residues: 948-1049 <ALL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 809-947 < DEW2>
R; Allmann, H.; Fietzek, P.P.; Glanville, R.W.;
Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868,
A; Title: The covalent structure of calf skin ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A;Tille: The covalent structure of calf skin type III c
A;Reference number: A38004; MUID:80026030; PMID:488910
A;Accession: A38004
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Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832,
A;Title: The covalent structure of calf skin ty
A;Reference number: A38001; MUID:80026027; PMII
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A, Accession: A38001
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nilarity 26.5%;
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                                            Score 154.5; DB 1;
Pred. No. 0.0036;
); Mismatches 74;
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PAGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGGRGPPGSNGNPGPPGSSGAPGKDG

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A;Residues: 1-1670 <MAR>
A;Cross-references: GB:X80031; NID:g577563; PID:g577564
A;Experimental source: kidney
R;Turner, N.; Mason, P.J.; Brown, R.; Fox, M.; Povey, S.; Rees, A.; Pusey, C.
Clin. Invest. 89, 592-601, 1992
A;Title: Molecular cloning of the human Goodpasture antigen demonstrates it A;Reference number: A43928; MUID:92147878; PMID:1737849
A;Accession: A43928
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A;Mccession: A44043
A;Mccession: A44043
A;Mccession: A486-1670 <QUI>
A;Mcsidues: 1386-1670 <QUI>
A;Cross-references: GB:M92993; NID:g177895; PIDN:AAA21610.1; PID:g177896
A;Cross-references: GB:M92993; NID:g177895; PIDN:AAA21610.1; PID:g177896
A;Note: sequence extracted from NCBI backbone (NCBIP:115597)
A;Note: sequence extracted from NCBI backbone (NCBIP:115597)
A;Quinones, S.; Bernal, D.; Garcia-Sogo, M; Elena, S.F.; Saus, J.
J. Biol. Chem. 269, 17358; NUID:99274734; PMID:8006044
A;Contents: annotation; erratum; correction to intronic sequence in A4404
A;Contents: annotation; erratum; correction to intronic sequence in A4404
A;Centents: annotation; erratum; correction to intronic sequence in A4404
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C;Date: 28-Oct-1994 #sequence revision 03-Oct-1995 #text change 22-Jun-1999
C;Accession: A54763; A43928; Ā44043; A45971; A39786
R,Mariyama, M.; Leimonen, A.; Mochizuki, T.; Tryggvason, K.; Reeders, S.T.
J Biol. Chem. 269, 23013-23017, 1994
A;Title: Complete primary structure of the human alpha3(IV) collagen chain.
A;Reference number: A54763; MUID:94364994; PMID:8083201
A;Accession: A54763
                                                                                                                                                                                                                                                                                   A; Note: sequence extracted from NCBI backbone (NCBIP:133363); R; Morrison, K.E.; Mariyama, M.; Yang-Feng, T.L.; Reeders, S.T. Am. J. Hum. Genet. 49, 545-554, 1991
A; Title: Sequence and localization of a partial cDNA encoding A; Reference number: A39786; MUID:91153570; PMID:1882840
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R;Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.;
J. Biol. Chem. 267, 19780-19784, 1992
A;Title: Exon/intron structure of the human alpha 3(IV) ge
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A;Residues: 1331-1524,'I',1526-1670
A;Cross_references: GB:M81379
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A;Molecule type: mRNA A;Residues: 1453-1593, 'A',1595-1670 <MOR> A;Residues: 1453-1593, 'A',1595-1670 <MOR> A;Cross-references: GB:S55790; NID:g234418; PIDN:AAB19637.1; A;Crosment: Prolines and lysines at the third position of the ed and subsequently O-glycosylated.
C;Comment: In Goodpasture's syndrome, an autoimmune response
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A; Residues: 1427-1444 <BER>
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                                                                                                                                                                                                                                                        Accession: A39786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reference number: A44043; MUID:93015826; PMID:1400291
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Alternate names: Goodpasture antigen; procollagen al
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F;1154-1156/Region: cell attachment (R-G-D) motif
F;1306-1308/Region: cell attachment (R-G-D) motif
F;1345-1347/Region: cell attachment (R-G-D) motif
F;1432-1434/Region: cell attachment (R-G-D) motif
F;1432-1434/Region: cell attachment (R-G-D) motif
F;1431-151/Domain: carboxyl-terminal nonhelical, NC1 <NC1>
F;1451-1551/Domain: collagen IV carboxyl-terminal repeat <CT1>
F;1561-1665/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;1561-1661/Domain: collagen IV carb
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C;Keywords: alternative splicing; basement membrane; cell binding; coiled coil; extrace
E;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1670/product: collagen alpha 3(IV) chain, long splice form #status predicted <MAT>
E;29-42/Domain: amino-terminal nonhelical, NH1 <NH1>
F;43-1438/Region: interrupted helical
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Best Local :
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1306 RGDPGF-QGFPGVKGEKGNPGFLGSIGPPGPIGPKGPPGV 1344
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                                                                               AADPPFCPHYEKVSGDYGHPVYIVQDGP----PQSPPNI
                                                                                                                                                                       SPGAPGPPGPPGSHVIGIKGDKGSMGHPGPKGPPGTAGDMGPPGRLGAPGTPGLP--
                                                                                                                                                                                                                                                                                                                                                                                                                    EPGKENLPGDPTSNATSRGAEGFLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRA
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                                                                                                                                                                                                                                                          KPSESRHPGP-----
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Pred. No. 0.007
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collagen 2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 C;Accession: B31219; T37289; T26033; T37288 R;Kramer, J.M.; Cox, G.N.; Hirsh, D. Cell 30, 599-606, 1982

#text_change

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A;Cross-references: EMBL:AF022985; PIDN:AAB69961.1; GSPDB:GN00023; CESP:T15B7.4
A;Experimental source: strain Bristol N2; clone T15B7
C;Genetics:
                                                                                                                                                                                                                                                      R;Pauley, A.; Gattung, S.
R;Pauley, September 1997
submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                         A;Description: The sequence A;Reference number: Z21139 A;Accession: T32248
                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T15B7.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #t.
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R;Kramer, J.M.; Cox, G.N.; Hirsh, D.
J. Biol. Chem. 260, 1945-1951, 1985
J. Title: Expression of the Caenorhabditis elegans collagen genes A;Reference number: 221668; MUID:85105075; PMID:2578467
A;Recession: T37288
A; Introns: 266, C; Superfamily:
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A; Introns: 94/1
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A; Residues: 1-301 < K
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A; Residues: 1-301 < KRA>
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A; Reference
                                         A; Map position:
                                                                    A; Gene: CESP:T15B7.4
                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-325 < PAU>
                                                                                                                                                                                                   A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                           C; Accession: T32248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-301 < KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: T26033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Coles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: V00148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71tle: Comparisons of the complete sequences of two collagen genes from Caenorhabditis;
Reference number: A30826; MUID:83050944; PMID:7139711
;Accession: B31219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 GQSPRGGAVPRKFVSEMPMERDRG------AAHSLEPGKENLPGDPT--SNATSRGAE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLGLGGGGGMGPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPAGPAGNDGAPGAPGG-----PGEPGASEQGGP-----GEPGPAGPAGPAGNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPLPPPSMPAVAGAAGGLALLLLGVAGA----GGAMCWRRRRAKPSESRHPGP-GSFGRGG
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                     266/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .-301 <KR3>
unassigned
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.2%; Score 151.5; DB 2;
28.7%; Pred. No. 0.0015;
15. Mismatches 72;
  collagens
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                                                                                                                                                                                                                                                                                                                                                               29-Oct-1999 #text_change
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hypothetical protein F02D10.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te) C;Accession: T20497 R;Swinburne, J.
                                                                                                                                RESULT 20
T20497
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submitted to the EMBL Data Library, March 1994
A;Description: A novel collagen encoding mRNA is transiently accumulated during ecdyson
A;Reference number: $42886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-569 <CHA>
A;Cross-references: EMBL:Z30348; NID:g457768; PIDN:CAA83002.1; PID:g457769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Bombyx mori (silkworm)
C;Date: 06-Jan-1995 #sequence_rev
C;Accession: $42886
R;Chareyre, P.P.; Besson, M.M.; F
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submitted to the EMBL Data Library, A;Reference number: Z19283
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Best Local Similarity
Matches 92; Conserv
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                                                                                                                                                                                                                                              GPREAEPGELGIALRG----GGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                    QAG-----QPGYPGQGG-----QPIKPAQPGHPGQPGQPGQPGTPGQPGQPGYPGQPGQ
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                                                                                                                                                                                                          PGQPGQPGQQGYPGQGGPQQGGQPINPSQPGYPGQSGQPGYPGQPVQPGQPGQP
                                                                                                                                                                                                                                                                                                                        AAGGLALLLIGVAGAGGAMCWRRRRAKPSESRHPG-----PGSFGRGGSLGLGGGGGGM 283
                                                                                                                                                                                                                                                                                                                                                              PGQGGQPIKPGQ-----PGYPGQPGQPGQPGYPGQP-GQPGAPGQPGQPGQPGQPGTPG 50
                                                                                                                                                                                                                                                                                                                                                                                                PRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQG--GVCLTRGMKVLLRVGQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRARPPGPHSSPNYEFYKLYLVG------GAQGRRCEA-PPAPNLLLTCDRPDLDL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSASTLVTVASAASGIAIVVCVFTVGMIFNDINSFYDEKIGELKEFKGYEQIA--WQAMI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PGQPGAPGEQGHPG-----LAGQPGSGARINPATGRPGFCIT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 149; DB 2;
Pred. No. 0.0045;
4; Mismatches 7'
                      November 1995
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                                                                          #text_change
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R;Rokos, I.; Muragaki, Y.; Warman, M.; Olsen, B.R.
Matrix Biol. 14, 1-8, 1994
A;Title: Assembly and sequencing of a cDNA covering the entire mouse alpha-1(IX) collage
A;Reference number: S42617; MUID:94340199; PMID:8061915
A;Accession: S42617
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C;Species: Mus musculus (house mouse)
C;Date: 25-De_____ #sequence_revision 19-Apr-1996 #text_change 20-Sep-1999
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A;Status: preliminary; translated
A;Molecule type: DNA
A;Molecule type: DNA
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A;Experimental source: clone F02D10
                                              8
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Best Local S
Matches 87
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                                                                                GIPGAAGDQGQRGPPGETGPEGDRGI-----QGSRGIPGSPGPKGDTGLPGVDGRDGIPG 550
                                                                                                                                                                                                                                                                                        AVP-----RKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATS--RGAEGPLPPPS 224
                                                                                                                                                                                                                                                                                                                                                    ----PGRQGHKGEEGDQGELGEVGDQGPPGPQGLRGITGIVGDKGEKGARGFDGEPGPQ 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPNSCPPGRSGYPG-----LPGMRGHKGAKGEIGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPP--GPPGPS-----GTIGFHDG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSGSAGGPGPKGPPGPAGQPGSDGNPGTAGPPGNPGGEGEKGICPKYCAIDG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLGGGGGMGPR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDP-----TSNATSRGA 216
   PPGEVGPRGPRGLPGSRGPVGPEGSPGIPGKLGSVGSPGLPGLPGPPGLPGMKGDRGVFG
                                                     -PGSFGRGGSLGL-GGGGGMGPREAE--PGELGIALRGG--GAADPPFCPHYEKVSGDYG 319
                                                                                                                                                                        MPAVAGAAG-----SLALL--LLGVAGAGGAMCWRRRRAKPSE-----SRHPG---
                                                                                                                                                                                                                                                                                                                                                                                                         FQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQG--GVCLTRGMKVLLRVGQSPRGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPRARPPGPHSSPNYEFYKLYLVG-----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGPAGPPGNDGQPGQPGGPG--QDGASSAGG-----EAGPGPAGPPGPAGPPGPDGQS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP-GSFGRGGSL 275
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Conservative
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24.0%; Pred. No. 0.009;
ive 23; Mismatches 130; Indels 1
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28.5%; Pred. No. 0.00
ive 12; Mismatches
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                                                                              F.842-874/Domain: collagenous #status predicted F;887-910/Domain: collagenous #status predicted F;887-910/Domain: collagenous #status predicted F;892-894/Region: cell attachment (R-G-D) motif F;918-969/Domain: collagenous #status predicted F;983-1000/Domain: collagenous #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 28-687,1', 689-734,'F',736-751,'R',753-1315 <OHW>
A;Residues: 28-687,1', 689-734,'F',736-751,'R',753-1315 <OHW>
A;Cross-references: EMB::L22545; NID:g348966; PIDN:AAA19787.1; PID:g511298
A;Cross-references: EMB::L22545; NID:g348966; PIDN:AAA19787.1; PID:g511298
A;Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 4229-4233, 1994
A;Title: Isolation and sequencing of cDNAs for proteins with multiple domains of Gly-Xa.
A;Reference number: A58370; MUID:94240111; PMID:8183893
A;Accession: S65595
                                                                                                                                                                                                                             F;364-437/Domain: collagenous #status F;462-583/Domain: collagenous #status F;607-689/Domain: collagenous #status F;704-745/Domain: collagenous #status F;759-831/Domain: collagenous #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:L22545
C;Comment: Prolines and lysines at the third position of the tripeptide repeating lated and subsequently O-glycosylated.
Lated and subsequently O-glycosylated.
C;Comment: The different splice forms of collagen alpha 1(XVIII) may be involved in C;Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action cap be useful in treating solid tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L16898; NID:g404754; PIDN:AAA37434.1; PID:g553894 R;Ch, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, submitted to the EMBL Data Library, August 1993 A;Reference number: S72450 A;Accession: S72450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:U11636; NID:g618427; PIDN:AAC52178.1; PID:g618428 R;Rehn, M.; Pihlajaniemi, T. Proc. Natl. Acad. Sci. U.S.A. 91, 4234-4238, 1994 A;Title: Alpha1(XVIII), a collagen chain with frequent interruptions in the collagenous A;Reference number: A58371; MUID:94240112; PMID:8183894 A;Accession: A58371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R,Rehn, M.; Pihlajaniemi, T.
J. Biol. Chem. 270, 4705-4711, 1995
A,Title: Identification of three N-terminal ends of type
tif homologous to rat and Drosophila frizzled proteins.
A,Reference number: A56101; MUID:95181468; PMID:7876242
A;Accession: A56101
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C; Superfamily: unassigned collagens
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A; Residues: 28-1315 < OHS>
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A; Residues: 1-928 < REH2>
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   F;126,488/Binding
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A;Residues: 1-103 <REH1>
                                                                                                                                                                                                                                                                                                                                                                                                         ;Keywords: alternative splicing; angiogenesis inhibitor; ,1-25/Domain: signal sequence #status predicted <SIGo; ,24-235/Region: thrombospondin amino-terminal similarity; ,26-1315/Product: collagen alpha 1(XVIII) chain, short sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Date: 03-Oct-1995 #sequence revision 08-May-1998; Accession: A56101; A58371; $72450; $65595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Mus musculus (house mouse)
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                                                                                                                                                                  26-1315/Product: collagen alpha 1(XVIII) chain, short 237-353/Domain: collagenous #status predicted <CO1>364-437/Domain: collagenous #status predicted <CO2>462-583/Domain: collagenous #status predicted <CO3>607-689/Domain: collagenous #status predicted <CO4>704-745/Domain: collagenous #status predicted <CO5>759-831/Domain: collagenous #status predicted <CO5>842-874/Domain: collagenous #status predicted <CO5>842-874/Domain: collagenous #status predicted <CO5>867-910/Domain: collagenous #status predicted <CO5>867-910/Domain: collagenous #status predicted <CO8>
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   site: carbohydrate
                               endostatin #status predicted <EST>
nultiplexin collagen carboxyl-terminal similarity
   (Asn)
(covalent) #status predicted
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B.R.

#status

predicted

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A; Note: this sequence is presented as substitutions relative to another sequence in a fies they replace; the appropriate interpretation of the sequence figure was reconstructed C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix C; Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix F; 37-96/Domain: you willebrand factor type C repeat homology < VWC>
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A;Molecule type: mRNA
A;Residuss: 1-1492 <SUA>
A;Cross-references: GB;M63596
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                                                                                                                                             PRGGAVPRKPVSEMPMERDRG-AAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVA 229
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                                                 GLGGNFAAQMTGGFDEKAGGAQMGVMQGPMGPMGPRGPPGPSGAPGPQGFQGNPGEPGES
                                                                               GAAGGLALLLLG -- VAGAGGAMCWRRR-----
                                                                                                            PRGPPGPQGPSGEQGPRGERGDKGETGAPGPRGRDGEP----GTPGNPGPAGPPGPPGPP 178
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Pred. No. 0.019
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 -GAADPPFCPHYEKVSGDYGHP
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A;Molecule type: protein
A;Residues: 1591-1610 <ORE>
A;Residues: 1591-1610 <ORE>
A;Residues: 1591-1610 <ORE>
A;Residues: Inhibits endothelial cell proliferation
C;Comment: Prolines and lysines at the third position of the tripeptilated and subsequently O-glycosylated.
C;Comment: The different splice forms of collagen alpha 1(XVIII) may
C;Comment: Endostatin is released from collagen alpha 1(XVIII) chain ay be useful in treating solid tumors.
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A;Molecule type: DNA; mRNA
A;Rolecule type: DNA; mRNA
A;Residues: 1293-1403,'R',1405-1774 <REH3>
A;Cross-references: GB:U03714; NID:g487733; PII
A;Cross-references: GB:U03714; NID:g487733; NID:g48774; NID:g48774; NID:g48774; NID:g48774; NID:g48774; N
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R;Abe, N.; Muragaki, Y.; Yoshioka, H.; Inoue, H.; Ninomiya, Y.
Biochem, Biophys. Res. Commun. 196, 576-582, 1993
A;Title: Identification of a novel collagen chain represented
A;Reference number: PN0675, MUID:94059075; PMID:8240330
A;Accession: PN0675
A;Molecule type: mRNA
A;Residues: 635-1774 <ABE>
A;Rein, M.; Hintikka, E.; Pihlajaniemi, T.
U. Biol. Chem. 269, 13929-13935, 1994
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A;Residues: 487-1146,'L',1148-1193,'F',1195-1210,'R',1212-1512,'L',1514-1522,'F',
A;Residues: 487-1146,'L',1148-1193,'F',1195-1210,'R',1212-1512,'L',1514-1522,'F',
A;Cross-references: RMBL:L22545, NID:g348968; PION:AAA19787,1; PID:g511298
R;Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 4229-4233, 1994
A;Title: Isolation and sequencing of cDNAs for proteins with multiple domains of A;Reference number: A58370; MUID:94240111; PMID:8183893
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A;Experimental source: splice form clones PE8.1,
R;Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons,
submitted to the EMBL Data Library, August 1993
A;Reference number: S72450
A;Accession: S72450
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J. Biol. Chem. 270, 4705-4711, 1995
A;Title: Identification of three N-terminal ends of type XVIII collagen chains tif homologous to rat and Drosophila frizzled proteins.
A;Reference number: A56101; MUID:95181468; PMID:7876242
A;Accession: B56101
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C;Date: 03-Oct-1995 #sequence_revision 08-May-1998 #text_change 31-Mar-2000
C;Accession: B56101; C56101; S72450; S65595; PN0675; A54072; A58816
                               A;Gene: MGI:Coll8a1
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A; Residues: 487-1512,'L',1514-1522,'F',1524-1683,'V',1685-1774
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ell 88, 277-285, 1997
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ai, N.; Vasios, G.
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G.; Lane, W.S
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C.Superfamily: unassigned collagens
C.Superfamily: unassigned collagens
C.Superfamily: unassigned collagens
C.Superfamily: unassigned collagens
F;1-274/Product: collagen alpha 1(XVIII) chain precursor, long splice form #status pred
F;1-239,487-1774/Product: collagen alpha 1(XVIII) chain precursor, medium splice form #s
F;1-24/Domain: signal sequence #status predicted <CO01>
F;181-486/Region: frizzled similarity
F;786-812/Domain: collagenous #status predicted <CO02>
F;281-1042/Domain: collagenous #status predicted <CO03>
F;1066-1148/Domain: collagenous #status predicted <CO04>
F;1016-124/Domain: collagenous #status predicted <CO06>
F;1010-123/Domain: collagenous #status predicted <CO06>
F;1010-133/Domain: collagenous #status predicted <CO06>
F;1010-133/Domain: collagenous #status predicted <CO08>
F;1011-133/Domain: collagenous #status predicted <CO08>
F;1042-135/Region: collagenous #status predicted <CO08>
F;1042-135/Region: collagenous #status predicted <CO08>
F;1042-1459/Domain: collagenous #status predi
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A; Introns: 1;
A; Note: the 1
C; Superfamily
C; Keywords: 5
F; 1-1774/Prod
collagen alpha 3(IX) chain precursor - chicken c/Species: Gallus gallus (chicken)
C/Species: Gallus gallus (chicken)
C/Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change 20-Sep-19
C/Accession: $20819; $22419; $22218; $22238; $C18856; $22241
R/Brewton, R.G.; Ouspenskaia, M.V.; van der Rest, M.; Mayne, R.
Eur. J. Biochem. 205, 443-449, 1992
A/Title: Cloning of the chicken alpha-3(IX) collagen chain completes the A/Reference number: $20819; MUID:92241276; PMID:1572350
A/Residues: 1-675 cBRE>
A/Residues: 1-675 cBRE>
A/Rosession: S20819
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Best Local (
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Note: the list of introns is incomplete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKVSGDYGHPVYIVQ-----DGPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GDVGIPGPKGSKGDLGPIGMPGKSGLA---GSPGPVGPPGPPGPPGPPGPPGFAAGF 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAKPSESRHPGP-GSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG--GAADPPFCPHY 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGPAGLPGVP-----GKEGPPGFPGFPGPPGPPGKEGP----PGVAGQKGSV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKGEKGDPGIGPRGPPGP------90PPGPSFRQDKLTFIDME 908
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A;Accession.
A;Molecule type: protein
A;Residues: 540-548 <MAY>
R;Ninomiya, Y.; van der Rest, M.;
R;Ninomiya, Y.; van der Rest, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Har-El, R.; Sharma, Y.D.; Aguilera, A.; Ueyama, N.; Wu, J.J.; Eyre, D.R.; Jurici J. Biol. Chem. 267, 10070-10076, 1992
A;Title: Cloning and developmental expression of the alpha3 chain of chicken type A;Reference number: S22429; MUID:92250566; PMID:1577778
A;Accession: S22429; MUID:92250566; PMID:1577778
A;Accession: S22429; MUID:92250566; PMID:1577778
A;Residues: 1-195,'G',197-675 <HAl>
A;Residues: 1-195,'G',197-675 <HAl>
A;Cross-references: EMBL:M83179
A;Cross-references: EMBL:M83179
A;Gross-references: EMBL:M83179
A;Gross-reference
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A;Residues: 1-195,'G','197-405,'S',407-675 <HA2>
A;Residues: 1-195,'G','197-405,'S',407-675 <HA2>
A;Cross-references: EMBL:M83179; NID:g211040; PIDN:AAB59960.1;
R;Mayne, R.; van der Rest, M.; Ninomiya, Y.; Olsen, B.R.
Ann. N. Y. Acad. Sci. 460, 38-46, 1985
A;Title: The structure of type IX collagen.
A;Reference number: S22238; MUID:86185164; PMID:3868958
A;Accession: S22238
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A;Title: The structure and macromolecular organization of type IX coll. A;Reference number: S22241; MUID:90247791; PMID:2186687
A;Accession: S22241
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A;Title: Construction and characterization of cDNA encoding the alpha2 chain A;Reference number: A18856; MUID:86026268; PMID:2996593
A;Accession: C18856
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A; Residues: 135, 'E', 137-187, 'X', 189-191 <SHI>
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A; Residues: 540-558 <NIN>
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3,22-675/Product; collagen alpha 3(IX) chain #status predicted <NAT>
3,22-24/Domain: non-collagenous NC4 #status predicted <NC4>
3,25-161/Domain: collagenous COL3 #status predicted <COL3>
3,102-176/Domain: non-collagenous NC3 #status predicted <NC3>
3,177-515/Domain: non-collagenous NC2 #status predicted <NC3>
3,516-546/Domain: collagenous NC1 #status predicted <NC2>
3,547-657/Domain: non-collagenous NC2 #status predicted <NC1>
3,658-675/Domain: collagenous COL1 #status predicted <NC1>
3,658-675/Domain: non-collagenous NC1 #status predicted <NC1>
3,137,443,146,149,152,155,179,182,185,552,558/Modified site: hydroxyproline (Pr
3,137,443,146,149,152,555,179,182,185,155,558/Modified site: hydroxyproline (Pr
3,170,174,525,658,663/Disulfide bonds: interchain #status predicted
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Best Local
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                                                                                                                                                                           PGPPGPPGPSGLPGGNGFRGPPGPSGLPGFPGPPGPPGLAGIIPEGGGDLQCPALCP 175
                                                                              -GAADPPFCPHYEKVSGDYGHPVYIVQDGP----PQSPPNI 336
                                                                                                                                                                                                                                                                                                                                                  PGAAGEAGLPGLP----GVDGLTGT-----DGPPGPNGPPGDRGALGPAGPPGPAGKGL
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R;McMurray, A.
submitted to the EMBL Data Library, Nov
A;Reference number: Z19345
A;Accession: T20906
A;Status: preliminary; translated from
                                                                                                                              R;Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P. Biochem. J. 273, 141-148, 1991
A;Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen. A;Reference number: S13301; MUID:91113131; PMID:1703407
A;Recession: S13301
                                                                                                                                                                                                                      collagen alpha 1(X) chain precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999

C;Accession: S13301
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A;Introns: 27/3; 49/3
C;Superfamily: unassigned
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A;Residues: 1-305 <WIL>
A;Cross references: EMBL:Z81503; PIDN:CAB04111.1; GSPDB:GN00021; CESP:F14F7.1
A;Experimental source: clone F14F7
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  A;Gene: COL10A1
C;Superfamily: coli
C;Keywords: coiled
                                                                          A;Molecule type: mRNA
A;Residues: 1-674 <THO>
A;Cross-references: EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revi
C;Accession: T20906
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33; Conservative
    collagen alpha 1(VIII) chain; c
iled coil; extracellular matrix;
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A; Molecule type: mRNA
A; Residues: 580-596, 598-620, 'R', 622-813; 835-884 <KIM>
A; Residues: 580-596, 598-620, 'R', 622-813; 835-884 <KIM>
R; Muragaki, Y.; Nishimura, I.; Henney, A.; Ninomiya, Y.;

proc. Natl. Acad. Sci. U.S.A. 87, 2400-2404, 1990

A; Title: The alpha1(IX) collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen gene gives rise to two calls of the collagen general general
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A;Residues: 1-253,'V',255-815;835-884 <NIN>
R;Kimura, T.; Mattei, M.G.; Stevens, J.W.; Goldring, M.B.; Ni Bur. J. Biochem. 179, 71-78, 1989
A;Title: Molecular cloning of rat and human type IX collagen A;Reference number: S02140; MUID:89137096; PMID:2465149
A;Accession: S02140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha 1(IX) chain precursor, long splice form - N;Alternate names: procollagen alpha 1(IX) chain, long sp c;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence revision 10-Feb-1995 #text c;Accession: S13580; S2325; S02140; C35980; S21087; S742

R;Muragaki, Y.; Kimura, T.; Ninomiya, Y.; Olsen, B.R.

Bur. J. Biochem. 192, 703-708, 1990

By T. J. Biochem. 192, 703-708, 1990

By T. J. Sinchem. 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKPGLPGLKGQRGPVGLPGSPGAKGEQGPAGHPGEAGLPGPSGNMGPQGPKGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----RPPGP-----HSSPNYEFYKLYLVG------GAQGR-RCEAPPAPNLLLT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALLLLMSLNLVHG-----VFY---TERYQTPTG-IKGPPSNTKTQFFIPYAIKGKGVSLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LRG-GGAADPPFCPHYEKVSGDYGHPVYIVQDGP----
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Boyd C.D., eds., pp.79-114, Academic with short triple-helical domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 674;
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$74294
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F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-931/Product: collagen alpha 1(IX) chain, long splice form #stat
F;24-288/Domain: non-collagenous NC4 #status predicted <NC4>
F;269-405/Domain: non-collagenous NC3 #status predicted <NC03>
F;406-417/Domain: non-collagenous NC3 #status predicted <NC3>
F;418-756/Domain: collagenous NC2 #status predicted <NC2>
F;418-756/Domain: non-collagenous NC2 #status predicted <NC2>
F;757-786/Domain: non-collagenous NC1 #status predicted <NC2>
F;787-901/Domain: non-collagenous NC1 #status predicted <NC1>
F;902-931/Domain: non-collagenous NC1 #status predicted <NC1>
F;1071/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gross-references: GDB:119794; OMIM:120210
A;Map position: 6912-6914
A;Introns: 5/2; 232/3; 260/3; 267/3
A;Introns: 5/2; 232/3; 260/3; 267/3
G;Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2(G;Function:
A;Description: structural component of extracellular fibrous polymer associated with type A;Note: in chondrocytes the long splice form is predominantly produced
A;Note: in chondrocytes the long splice form is predominantly produced
C;Superfamily: unassigned collagens
C;Superfamily: unassigne
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A; Residues: 405-417 < DIA>
C; Comment: Prolines and l;
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A;Molecule type: DNA
A;Residues: 1-4;233-267 <MUR2>
A;Cross-references: EMBL:M32135
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Best Local S
Matches 84
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Cross-references: EMBL:M32135
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   SLGSPGLPGLPGPPGLP
                                                                   DYGHPVYIVQDGPPQSP 333
                                                                                                                                      VAGEKGSTGAPGKPGQMGNSGKPGQQGPPGEVGPRGPQGLPGSRGELGPVGSPGLPGKLG
                                                                                                                                                                                                                 LGGGGGMGPREAEPGELGIALRGG-----
                                                                                                                                                                                                                                                                                    GLPGPKGDTG-----LPGVDGRDGIPGMPGTKGEPGKPGPPGDAGLQGLPGVPGIPGAKG 583
                                                                                                                                                                                                                                                                                                                                                    SMPAVAGAAGGLALLILGVAGAGGAMCWRRRRAKPSESRHPG-----PGSFGRGGSLG 276
                                                                                                                                                                                                                                                                                                                                                                                                                           GLRGITGLVGDKGEKGARGLDGEPGPQGLPGAPGDQGQRGPPGEAGPKGDRGAEGARGIP 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRKPVSEMPMERDRGAAHSL--EPGKENLPGDPTSNAT-----SRGAEGPLPPP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAV 176
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22.3%; Pre
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Pred. No. 0.015;
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A; Molecule type: protein
A; Residues: 1-90;91-254;255-304;305-374;375-438 <GAI>C; Superfamily: unassigned collagens
C; Keywords: coiled collagens
                                                                                                                                                                              A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-95,'X','97-107,'X',109-191,'X',193-260,'X',262-278,'X',280-572,
A;Rote: we have shown the unidentified residues as Lys forming glycosylated
A;Mann, K.; Gaill, F.; Timpl, R.
submitted to the Protein Sequence Database, July 1992
A;Description: Amino acid sequence and cell adhesion activity of a fibril-fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collagen alpha chain - tube worm (Riftia pachyptila) (fragment) (Species: Riftia pachyptila (Species: Riftia pachyptila (Species: Riftia pachyptila (Spate: 22-Nov-1993 #sequence revision 09-Mar-1996 #text_change (Spate: 22-Nov-1993 #sequence revision 09-Mar-1996 #text_change (Spate: S28774; S22915; S17581 R,Mann, K.; Gaill, F.; Timpl, R.
Eur. J. Biochem. 210, 839-847, 1992 A,Title: Amino-acid sequence and cell-adhasion activity of a fik A,Reference number: S28774; MUID:93130909; PMID:1483468
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R;Gaill, F; Mann, K.; Wiedemann, H.; Engel, J.; Timpl, R.
J. Mol. Biol. 246, 284-294, 1995
A;Title: Structural comparison of cuticle and interstitial
A;Reference number: S53786; MUID:95173973; PMID:7869380
A;Accession: S53787
A; Molecule type: protein A; Molecule type: protein A; Molecule type: 1-95, 1^{\circ}, 1^{\circ
                                                                                                                                                                A;Description: Amino acid sequence
A;Reference number: S22915
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                                                                                                                            A;Accession: S22915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Species: Paralvinella grasslei
;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 07-May-1999
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 RGVPGALGPPGPQGERGLPGER---GLPGSRGPGGARGGPGERGPSGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
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Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                               .'X',574-611,
5-hydroxyly:
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collagen alpha-4 chain precursor - sea urchin (Strongylocentrotus N,Alternate names: collagen alpha 2 (IV) chain homolog C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 07-Uul-1995 #sequence revision 07-Uul-1995 #text_change 13 C;Accession: A54121; S44317 Geourjon, C.; Garrone, R.; Solursh, R.Exposito, J.Y.; Suzuki, H.; Geourjon, C.; Garrone, R.; Solursh, J. Biol. Chem. 269, 13167-13171, 1994
A;Title: Identification of a cell lineage-specific gene coding for A;Reference number: A54121; MUID:94230414; PMID:8175744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S17581
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 8-45;525-545,'X',547-566,'X',568-572,'X',574-611,'X',613-618;'X',811-882 <C
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
h 3- and 4-hydroxylated in the X-position. Lysines are 5-hydroxylated and subsequently
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Gaill, F; Wiedemann, H; Mann, K.; Kuehn, K.; Timpl, R.; Engel, J. J. Mol. 221, 209-223, 1991
A;Title: Molecular characterization of cuticle and interstitial collagens A;Reference number: S17581; MUID:92015209; FMID:1920405
A; Molecule type: mRNA
A; Residues: 1-1747 <EXP>
A; Cross-references: EMBL: X76730;
C; Genetics:
                                                     A; Reference number: A54121;
A; Accession: A54121
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mes 82; Conservative
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             NID: 9483606;
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Pred. No. 0.01:
4; Mismatches
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             PIDN:CAA54146.1; PID:g483607
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A;Accession: S23779
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C;Superfamily:
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C;Species: Mus musculus (house mouse)
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Best Local :
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family: collagen
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                                                                                      TSDGT----
                                                                                                                                                                                                                                                                                      101;
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                                                                                                                                                                                                                                                                                      Score 142.5; DB 1;
Pred. No. 0.017;
9; Mismatches 136;
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Pred. No. 0.04;
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C;Species: Mus musculus (nouse mouse, C;Species: Mus musculus (nouse mouse, C;Date: 10-Sep-1999 #text_C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_C;Date: 10-Sep-1999 #text_C;Date: S23779 #sequence_revision 10-Sep-1999 #text_C;Date: S23779; MUID: 92362626; PMID: 1499564
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GPPGPHGLPGIGKPGGPGLPGQPGAKG-ERGPKGPPGPPGLQGPKGEKGFGMLGLPGLKG
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A;Cross-references: GB:X04758; NID:g29588; PIDN:CAA28454.1; PID:g1340175
A;Experimental source: rhabdomyosarcoma cell line
R;Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M.
J. Biol. Chem. 260, 5533-5541, 1985
A;Title: Partial covalent structure of the human alpha 2 type V collagen cha.
A;Reference number: 155239; MUID:85182703; PMID:2985598
A;Reference number: 155239; MUID:85182703; PMID:2985598
A;Accession: 155239
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1002-1226 <RE2>
A;Cross-references: GB:M10956; NID:g180427; PIDN:AAA52007.1; PID:g180428
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A;Residues: 1-32 GRRs
A;Residues: 1-32 GRRs
A;Cross-references: GB:M58529; NID:g180834; PIDN:AAC41699.1; PID:g553235
A;Cross-references: GB:M58529; NID:g180834; PIDN:AAC41699.1; PID:g553235
A;Champliaud, M.F.; Boutillon, M.M.;
Bur. J. Biochem. 221, 987-995, 1994
A;Title: Diversity in the processing events at the N-terminus of type-V collagen.
A;Reference number: S43642; MUID:94237164; PMID:81818482
A;Accession: S43643
A;Status: .......A;Status: ......A;Status: ......A;Afatus: .....A;Afatus: ....A;Afatus: .....A;Afatus: ....A;Afatus: .....A;Afatus: .....A;Af
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A;Cross references: GB:JU04478; NID:g179697; PIDN:AAA51859.1;
A;Experimental source: placenta
R;Greenspan, D.S.; Lee, S.T.; Lee, B.S.; Hoffman, G.G.
Gene Expr. 1, 29-39, 1991
A;Title: Homology between alpha2(V) and alpha1(III) collagen
A;Reference number: A54555; MUID:92314691; PMID:1820205
A;Accession: A54555
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A;Residues: 288-291,'P',293-294,'X',296-297;606,'X',608-617 <MOR>
A;Residues: 288-291,'P',293-294, 'X',296-297;606,'X',608-617 <MOR>
R;Weil, D.; Bernard, M.; Gargano, S.; Ramirez, F.
Nucleic Acids Res. 15, 181-198, 1987
Nucleic Acids Res. 15, 181-198, 1987
A;Title: The pro alpha 2(V) collagen gene is evolutionarily related A;Reference number: A25874; MUID:87146331; PMID:3029669
A;Accession: A25874
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C;Date: J.Jul-1995 #sequence revision 28-Jul-1995 #text change 31-Dec-2000
C;Date: 31:427; A54555; S43643; A25874; I55239; I59025; A25374; A30017
C;Accession: A31427; A54555; S43643; A25874; I55239; I59025; A25374; A30017
R;Woodbury, D.; Benson-chanda, V.; Ramirez, F.
J. Biol. Chem. 264, 2735-2738, 1989
                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: I59025
A;Status: translate
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A; Residues: 1-463 < WO
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A,Title: Amino-terminal propeptide of human pro-alpha2(V)
A,Reference number: A31427, MUID:89123368; PMID:2914927
A,Recession: A31427
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;Residues: 398-1496 <WEI>
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RGPRGDPGTLGPPGPVGERGAPGNRGF--

169 QSPRG--GAV-PRKPVSEMFMERDRGAAHSLEPGKENLPG------DPTSNATSRGAE 217

PGSDGLPGPKGAQGERGPVGSSGPKGSQ 554

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F;00y=125/Region: Gell attachment (R-G-D) motif
F;901-3-505/Region: Gell attachment (R-G-D) motif
F;941-943/Region: Gell attachment (R-G-D) motif
F;1064-1066/Region: Gell attachment (R-G-D) motif
F;1064-1066/Region: Gell attachment (R-G-D) motif
F;1097-1099/Region: Gell attachment (R-G-D) motif
F;1097-1099/Region: Gell attachment (R-G-D) motif
F;1133-1135/Region: Gell attachment (R-G-D) motif
F;1251-1260/Region: Gell attachment (R-G-D) motif
F;1251-1496/Domain: Gell attachment (R-G-D) motif
F;1251-1496/Domain: Gell attachment (R-G-D) motif
F;1269-1496/Domain: Gell attachment (R-G-D) motif
F;127/Modified site: pyrrolidone carboxyl-terminal homology <FCC>
F;27/Modified site: pyrrolidone carboxyl: acid (Gin) (in mature form) #status predicted
F;194/Modified site: pyrrolidone carboxyl: acid (Gin) (in mature form) #status predicted
F;290,293,296,608,614,1004,1007,1013,1028,1034/Modified site: 4-hydroxypyrsine (Lys) #status predicted
F;299,1139/Modified site: 5-hydroxylysine (Lys) #status predicted
F;1025/Modified site: 5-hydroxylysine (Lys) #status experimental
F;1250-1251/Cleavage site: Glu-Asp (procollagen C-endopeptidase) #status predicted
F;1293,1299,1325/Disulfide bonds: interchain #status predicted
F;1333-1494,1402-1447/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Description: structural component of extracellular fibrous polymer associated with ce A, Note: may play a role in controlling the lateral growth of collagen I fibrils C, Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology C, Keywords: coiled coil. extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol F;1-26/Domain: signal sequence #status predicted <SIG> F,27-105/Droduct: collagen alpha 2(V) chain #status predicted <MAT> F,27-195/Domain: amino-terminal propeptide (uncleaved) #status predicted <NPP> F,27-108/Region: nonhelical F,40-99/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:119064; OMIM:120190
A;Map position: 2q31-2q31
A;Introns: 33/1, 812/3; 830/3; 848/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 1448/
A;Introns: 33/1, 812/3; 830/3; 848/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 1448/
C;Complex: type V collagen may be a homotrimer of alpha 1(V) chains (see PIR:CGHUIV), a alpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among the ength, is formed with desmosine cross-links made from lysine and allysine residues C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mENA
A;Rosidues: 1227-1417, ", ',1419-1437, 'S',1439-1496 cMYB>
A;Residues: 1227-1417, ", ',1419-1437, 'S',1439-1496 cMYB>
A;Rosidues: GB:M11718; NID:g180912; PIDN:AAA52058.1; PID:g180913
A;Experimental source: normal fibroblasts
R;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.;
Genomics 3, 275-277, 1988
A;Title: Genetic distance of two fibrillar collagen loci, COL3A1 and COLA; Reference number: A30017; MUID:89138450; PMID:3224983
A;Accession: A30017
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A;Residues: 1449-1463,'E',1465-1495,'A' <TSI>
A;Cross-references: GB:J03051; NID:g179695; PIDN:AAA51858.1; PID:g179696
A;Cross-references: GB:J03051; NID:g179695; PIDN:AAA51858.1; PID:g179696
A;Note: the authors translated the codon GAA for residue 1460 as GIn, and GAG for C;Comment: Prolines and lysines at the third position of the tripeptide repeating are 5-hydroxylated and subsequently O-glycosylated.
C;Comment: The amino-terminal propeptide domain appears not to be completely cleav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;109-186/Region: helical F;187-208/Region: nonhelical F;209-1225/Region: helical
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C;Genetics:
A;Gene: GDB:COL5A2
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J. Biol. Chem. 260, 11216-11222, 1985
A;Title: Complete primary structure of the human alpha-2 type V procollagen COOH-termin A;Reference number: A53374, MUID:85289337; PMID:2411731
A;Accession: A25374
                                        Similarity
                              7.7%; Score 142.5; DB 29.1%; Pred. No. 0.037;
                                                                                     DB 1;
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43;
Gaps
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RESULT
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C;Date: 13-Jan-1995 #text_change 13-
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-
C;Accession: S15435
R;Muragaki, Y:; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Ninomiya,
Bur. J: Blochem. 197, 615-622, 1991
A;Title: The complete primary structure of the human alpha-1(VIII)
A;Reference number: S15435; MUID:91231001; PMID:2029894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagen alpha 1(VIII) chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
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A;Molecule type: mRNA
A;Residues: 1-744 <MUR>
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Best Local S
Matches 73
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;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology;
;1-20/Domain: signal sequence #status predicted <SIG>
;21-744/Product: collagen alpha 1(VIII) chain #status predicted <WAT>
;21-117/Region: amino-terminal nonhelical
;118-571/Region: interrupted helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;572-744/Region: carboxyl-terminal nonhelical;672-744/Region: carboxyl-terminal homology
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                                                                                                                                                                                                                                                                             VAGAGGAMCWRRRRAKPSESRHPG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG 126
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                                                                                                       EGGIVGPQGPP
                                                                                                                                                                         RGMGGVPGALGPR-GEKGPIGSPGIGGSPGEPGLPGIP-
                                                                                                                                                                                                                                                                                                            ----PGMHGL-PGPVGLPGVGKPGVTGFPGPQGPLGKPGAPGEPGRQGPIGVPGVQGPPG
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                                                                                                                                        -----PQSPP 334
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73; Conserv
2(VI) chain precursor musculus (house mouse)
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Pred. No. 0.019;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  -LRGPKGDKGFGMPGAPGVKGP-
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A;Title: Structure of cDNAs encoding the triple-helical domain of murine alpha-2(VI) corate oligonuclectides for generation of novel cDNA clones.

A;Reference number: $13745; MVID:91226374; PMID:1709252

A;Recession: $13745

A;Rolecule type: mRNA
A;Crose-references: GB:L06343; NID:g192671; PIDN:AAA37441.1; PID:g192672
A;Crose-references: GB:L06343; NID:g192672; PIDN:AAA37441.1; PID:g192672
A;Crose-references: GB:L06343; NID:g192672
A;Crose-references: GB:L06344, NID:g192672
A;Crose-references: GB:L06344, NID:g192672
A;Crose-references: GB:L06344, NID:g192672
A;Crose-refere
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A;Cross-references: EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49809
R;Ibrahimi, A.; Bertrand, B.; Bardon, S.; Amri, E.Z.; Grimaldi, P.; Ailha
Blochem. J. 289, 141-147, 1993
A;Title: Cloning of alpha2 chain of type VI collagen and expression durin
A;Reference number: S28808; MUID:93143659; PMID:8380980
A;Accession: S28808
A;Accession: S28808
A;Residues: 266-1029 <IB2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: Zoo-IVEJ .... A; Cross-references: EMBL: X62332; A; Cross-references: C.D.; Jimenez, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --EFRSHHDYYIIATSDGTREGLESLQG--GVCLTRGMKVLL-RVG-QSPRGGAVPRKP- 180
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                                                                                                                                                                                                                     GDRGLPGPRGPQ-GALGEPGKQGSRGDP
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ilarity 29.7%;
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Pred. No. 0.027;
5; Mismatches 125; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SESRHPGP----GSFGRGGSLGLG
                                                                                                                                                                                                                           GDAGPRGDSGQPGPKGDPGRPG
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CGHU7L

Collagen alpha 1(III)

N,Alternate names: procollagen alpua -..

N,Alternate names: procollagen alpua -..

C;Species: Homo sapiens (man)

C;Date: 24-Apr-1984 #sequence revision 01-Sep-1995 #tf

C;Accession: S05272; S04642; PE0011; S01726; S04887;

R;Prockop, D.J.

submitted to the EMBL Data Library, February 1989
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A;Accession: S16366
A;Molecule type: mRNA
A;Residues: 1-1763 <JBI>
A;Cross-references: GB:M67
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 229/3; 266/3; 305/3; 360/3; 424/1; 489/1; 548/1; 656/3; 790/1; 891/1; 963/1; (Superfamily: collagen alpha 1(IV) chain
C;Reywords: alternative splicing; basement membrane; cell binding; coiled coil; disulfid
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-1763/Product: collagen alpha 2(IV) chain #status predicted <MAT>
F;27-42/Domain: non-collagenous MH1 #status predicted NH1>
F;43-1529/Domain: collagenous #status predicted <NH1>
F;197-199/Region: cell attachment (R-G-D) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen alpha 2(IV) chain precursor - pig roundworm (;Species: Ascaris suum (pig roundworm)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #t
C;Accession: $16366
R;Pettitt, J.; Kingston, I.B.
J. Biol. Chem. 266, 16149-16156, 1991
A;Title: The complete primary structure of a nematod:
A;Reference number: $16366; MUID:91340768; PMID:1714;
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                                                                                                       ;1530-1638/Domain: repeat NC1 #status predicted <NC11>;1639-1763/Domain: repeat NC1 #status predicted <NC12>;1639-1763/Domain: repeat NC1 #status predicted <NC12>;31,34,39,41,536,539/Disulfide bonds: interchain #status predicted;126/Binding site: carbohydrate (Asn) (covalent) #status predicted;1593-1599,1702-1709/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPP--GPQGIK-GDRGIIGVPGFPGNDGANGRPGEPGPPGAPGWDGCNGTDGAPG----V 134
                                                                                                                                                                                                                                                                                                                                                              EF----SDGPP-GPPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRPGLPGPPGF---KGDRGLDGLPGVPGLPGQKGEAGFPGRDGAKGARGPPGPPG----GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG--GAADPPFCPHYEKVSG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMKGEKGDP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQAGPRGPPGBAGPPGNPGIGSIGPKGDPGEQGPRGPQGPPGPVPSTGAKGTIIGPEGAP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQIGDRLDLLCPRARP--PGPHSSPNYEFYKLYLVGGAQGRRCEA--PPAPNLLLTCDRP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPHSGPGGVRVGALLLLGVLGL----VSGLSLEP-----VYWNSANKRFQAEGGYVLY 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-----GLPGPPGMPGFPGPPGVPGMKGEPAIGYAGAPGEKGDAGMPGMPGL----- 181
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PMID:1714907
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399; A94562;
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                                                                                                                                    S59511;
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Biochem. J. 311, 939-943, 1995
A;Title: Abnormal type III collagen produced by an exon-17-skipping mutation A;Reference number: S59511; MUID:96067614; PMID:7487954
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A;Note: the authors translated the codon CAG for residue 154 as His
R;Naneczko, R.A.; Ramirez, F.
Nucleic Acids Res. 17, 6742, 1989
A;Telle: Nucleotide and amino acid sequences of the entire human alpha-1 (III)
A;Reference number: S04887; MUID:89386015; PMID:2780304
A;Accession: S04887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M26939; NID:g180813; PIDN:AAA52040.1; PID:g180
R;Toman, P.D.; Ricca, G.A.; de Crombrugghe, B.
Nucleic Acids Res. 16, 7201, 1988
A;Title: Nucleotide sequence of a cDNA coding for the amino-terminal
A;Reference number: S01726; MUID:88303360; PMID:3405773
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A;Note: the complete sequence is not shown
R;Benson-Chanda, V; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
Gene 78, 255-265, 1989
A;Title: Cloning and analysis of the 5' portion of the human type-III procollagen
A;Reference number: PE0011; MUID:89378752; PMID:2777083
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A; Title: Structure
                                                              A;Cross-references: GB:S62925; NID:g386425; R;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Biochem. J. 311, 939-943, 1995
                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: liver
A, Note: author submitted corrections to A90399
A, Note: author submitted corrections to A90399
R, Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, Am. J. Hum. Genet. 53, 62-70, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294-398 <SEY1>
A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: the authors' translation R; Seyer, J.M.; Kang, A.H. Blochemistry 16, 1158-1164, 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Nolecule type: mENA
A;Residues: 149-163,'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634
A;Cross-references: EMBL:X15332; NID:g59545; PIDN:CAA33387.1; PID:g930045
A;Note: the authors' translation of residues 905-932 is inconsistent with the nucleotid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S05272
A;Status: prelimina
                                                                                                                                                           A; Residues: 186-194 <MIL>
                                                                                                                                                                                  A;Status: preliminary; translated A;Molecule type: DNA
                                                                                                                                                                                                                                                           A;Reference number: I51868; MUID:93304430; PMID:8317500
A;Accession: I51868
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A;Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398
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A;Reference number: A94562
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A, Residues: 1-176 <BEN>
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A; Residues: 1-1196 < ALA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide;Reference number: A90399; MUID:77134724; PMID:557335
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                                                                                                                                                                                                                                                                                                                                             ;Title: Parental somatic
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                                                                                         PIDN:AAD13937.1; PID:g4261637 Bateman, J.F.
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A;Molecule type: mRNA
A;Residues: 950-1018,'Y',1020-1183,'S',1185-1466 <MANN>
A;Residues: 950-1018,'Y',1020-1183,'S',1185-1466 <MANN>
A;Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
R;Seyer, J.M.; Kang, A.H.
Blochemistry 20, 2621-2627, 1981
Blochemistry 20, 2621-2627, 1981
A;Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB9 from ty
A;Reference number: A90446; MUID:81208139; PMID:7016180
A;Recession: A90446
A;Molecule type: protein
A;Residues: 965-979,'A',981-984,'PS',987,'QN',990-1096,'P',1098-1152,'AT',1155,'S',1157-A;Experimental source: liver
R;Icoidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Mye
Nucleic Acids Res. 12, 9383-9394, 1984
A;Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollage
A;Accession: A93551; MUID:85087944; PMID:6096827
A;Accession: A93551; MUID:85087944; PMID:6096827
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A;Residues: 861-1015 <COL>
A;Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN:AAB59383.1; PI
A;Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos R;Mankoo, B.S.; Dalgleish, R.
Nucleic Acids Res. 16, 2337, 1988
A;Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.
A;Reference number: S02119; MUID:88189827; PMID:3357782
A;Accession: S02119
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A;Residues: 537-605 <LES>
A;Residues: 537-605 <LES>
A;Cross-references: GB.M59312; NID:g180815; PIDN:AAA52041.1;
R;Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589, 1980
A;Title: Covalent structure of collagen: amino acid sequence
A;Reference number: A90438; MUID:80198282; PMID:6246925
A;Accession: A90438
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A;Residues: 399-675,'N',677-727 <SEY3>
A;Residues: 399-675,'N',677-727 <SEY3>
A;Experimental source: liver
R;Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.;
J. Biol. Chem. 266, 5256-5259, 1991
A;Title: G to T transversion at position +5 of a splice
A;Reference number: I55349; MUID:91161621; PMID:1672129
A;Accession: I55349
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A; Residues: 1065-1155, 'P', 1157-1466 <LOI>
A; Residues: 1065-1155, 'P', 1157-1466 <LOI>
A; Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
A; Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
A; Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolsto:
Biochemistry 25, 1408-1413, 1986
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A;Residues: 728-895, A',897-964 <SEY4>
A;Residues: 728-895, A',897-964 <SEY4>
A;Reperimental source: liver
R;Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez,
J. Biol. Chem. 265, 17070-17077, 1990
A;Title: A base substitution at a splice site in the COL3Al gene
A;Cross-references: GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:g180416 R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C. Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
                                                                                                   A; Molecule type: mRNA
A; Residues: 1161-1200 < MIS>
                                                                                                                                                                                                       Biochemistry 25, 1408-1413, 1986
A;Title: Human type III collagen gene expression is coordinately modulated with the type
A;Reference number: I52393; MUID:86187804; PMID:3754462
A;Accession: I52393
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;Title: Covalent structure of collagen: amino acid sequence;Reference number: A90414; MUID:79000343; PMID:687591
;Accession: A90414
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Seyer, J.M.; Kang, A.H.
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A;Genericus:
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A;Cross-references:
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A;Title: Isolation of cDNA and genomic clones encoding human A;Reference number: A92516; MUID:85157600; PMID:2579949
A;Accession: A92516
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A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU's
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795;
A;Experimental source: liver
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A; Residues: 1165-1196 < EMA>
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A;Reference number: I59025; MUID:85216505;
A;Accession: I79359
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                                                               MPGPRGSPGPQGVKGESGKPGANGLSGERGPPGPQGLPGLAGTAGEPGRDGNPGSDGLPG
                                                                                                                                     KPSESRHPGP----GSFGRGGSLGLGG-GGGMGP---
                                                                                                                                                                                                 PPGPAGNTGAPGSPGVSGPKGDAGQPGEKGSPGAQGPPGAPGPLGIAGITGARGLAGPPG
                                                                                                                                                                                                                                                                                                                                                 PPGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGARGLPGPPGSNGNPGPPGPSGSPGKDG 903
                                                                                                                                                                                                                                                                                                                                                                                                                 PRGGAVPRKPVSEMPMERDRGA----AHSLEPGKENLPGDPTSNAT-----SRGAEG 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.6%;
llarity 27.6%;
Conservative 1:
GAADPPFCPHYEKVSGDYGHPVYIVQDGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 141.5; DB
Pred. No. 0.042;
3; Mismatches
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PMID:3858826
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                                                                                                                                                                                                                                                                           -ALLLLGVAGAGGAMCWRRRRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1466;
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Ramirez, F.
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J. Biol. Chem. 264, 16022-16029, 1999

A.Title: The cloning and sequencing of alphal(VIII) collagen cDNAs demonstrated comains similar to those of type x collagen.

A;Reference number: A34246; MUID:89380199; PMID:2476437

A;Accession: A34246

A;Accession: A34246

A;Molecule type: mRNA

A;Residues: 1-744 < YAM>

A;Cross-references: GB:JO5042; NID:g164895; PIDN:AAA31204.1; PID:g164896

C;Superfamily: collagen alpha 1 (VIII) chain; complement C1q carboxy1-terminal

F;11-20/Domain: signal sequence #status predicted <SIGS

F;21-744/Product: collagen alpha 1 (VIII) chain #status predicted <MAT>

F;21-71/Region: amino-terminal nonhelical

F;118-571/Region: interrupted helical

F;572-744/Region: carboxy1-terminal nonhelical

F;572-744/Region: carboxy1-terminal homology <C1Q>
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A;Reference number: 2
A;Accession: T32250
A;Status: preliminary
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A;Residues: 1-319 <PAU>
A;Coss-references: EMBL:AF022985; PIDN:AAB69959.1; GSPDB:GN00023; CESP:T15B7.3
A;Experimental source: strain Bristol N2; clone T15B7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 39
A34246
collagen alpha 1(VIII) chain precursor - rabbit
collagen elpha 1(VIII) chain precursor - rabbit
collagen conticulus (domestic rabbit)
Collage 10-Sep-1999 #sequence_revision 10-Sep-1999
Collage 10-Sep-1999
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A; Map position: 5
A; Introns: 266/1
C; Superfamily: unassigned collagens
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submitted to the EMBL Data Library, Septem
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/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
/Accession: 732250
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25.6%; Pred. No. 0.0088;
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-744 < MIN'
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
F;617-743/Domain: complement Clq carboxyl-terminal homology <ClQ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collagen alpha 1(VIII) chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: $22243
A; Accession: $23298
                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                               273
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   305 PP---FCPHYEKVSGDYGH---
                                                                                                           333 KGEQGLPGLPGPFGLPGVGKPGFPGPKGD-----RGIGGVPGALGPRGEKGPVGAPGMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 PPGPHGLPG-----IGKPGGPGLPGQPGAKGDRGPKGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                           67 PPGPHSSPNYEFYKLYLVG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                        KPSESRHPG-PGSFGRGGSLGL----GGGGGMGPR-----EAEPGELGIALRGG--GAAD
                                                                                                                                                                             PPGPHGLPG-----IGKPGGPGLPGQPGAKGDRGPKGPPGP------
                                    PPGEPGLPG1PGPMGPPGA1GFPGPKGEGG1VGPQGPPGPKGEPGLQGFPGKPGFLGEVG
                                                                                                                                           -----PGLQGPK------GEKGFGMPGLPGLKGPPGMHGPPGPVGLPGVG
                                                                                                                                                                                                                                                                                     IKFQEYSPNIWGHEFRSHHDYYIIATSDGTR----EGIESIQG--GVCLTRGMKVLLRVG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PP---FCPHYEKVSGDYGH------PVYIVQDGPP-----QSPPNI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPSESRHPG-PGSFGRGGSLGL----GGGGGMGPR----EAEPGELGIALRGG--GAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATSRGAEGPLPPPSMPAVA-----GAAGGLALLLLGVAGAGGAMCWRRRR------A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPGVTGFPGPQGPLGKPGPPGEPGPQGPLGVPGVQGPPGLPGVGKPGQDGLPGQPGFPGG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PGLQGPK------GEKGFGMPGLPGLKGPPGMHGPPGPVGLPGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKFQEYSPNLWGHEFRSHHDYYIIATSDGTR----EGLESLQG--GVCLTRGMKVLLRVG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPGPHSSPNYEFYKLYLVG------GAQG-RRCEAPPAPNLLLTCDRPDLDLRFT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPGIRGLPGPIGPKGEAGHKGLPGLPGVPGLLGPKGEPGIPGDQGLQGPPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPGPKGEPGLQGFPGKPGFLGEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGEQGLPGLPGPPGLPGVGKPGFPGPKGD-----RGIGGVPGALGPRGEKGPVGAPGMGG
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                            -----sprggavprkpvsempmerdrgaahslepgkenlpgdp---tsn
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                                                                                                                                                                                                                                                                                                                                                                                                                 7.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 141; DB 1;
Pred. No. 0.022;
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Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
 -PVYIVQDGPP-
                                                                                                                                                                                                                                                                                                                                                           -GAOG-RRCEAPPAPNLLLTCDRPDLDLRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                  108;
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                                                                                                                                                                                                                                                                                                                                                                                                Indels 132;
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OSPPNI
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PPGIRGLPGPIGPKGEAGHKGLPGLPGVPGLLGPKGEPGIPGDQGLQGPPGI

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C;Accession: T30165
R;Latreille, P.; Wamsley, P.; Kramer, J.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid
A;Reference number: Z20748
                                                       A; Map position:
a:Introns: 27/3
                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-304 <WIL>
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                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A; Reference number: Z19569
                                                                                                                                                                                                                                                                                                             hypothetical protein F52B11.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T22482
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A; Introns: 51/3; C; Superfamily: una
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U80444; PIDN:AAB37788.1; GSPDB:GN00019; CESP:F26B1.4 A;Experimental source: strain Bristol N2; clone F26B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-305 < LAT>
                                                                                                                                    A; Experimental source:
                                                                                                                                                      A;Cross-references: EMBL:Z82268; PIDN:CAB05195.1; GSPDB:GN00022;
                                                                                                                                                                                                                                 A;Reference number:
A;Accession: T22482
                                                                                                                                                                                                                                                                                             R; Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: F26B1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Introns: 51/3; 77/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ypothetical protein F26B1.4 - Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                       Superfamily:
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                                                                                                 CESP: F52B11.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIKFQEYSPNLWGHEFRSHHDYYIIATSDG-----TREGLESLQGGVCLTRGMKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQHFQETSEKIW-----DDLVFVATGETDRHKRHAYLTRAPVVPVTGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPGLAGAPGDSGAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPHYEKVSGDYGHPVYIVQDGPPQSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGEPGLPGPVGDPGFDGKPGNPGNNGVRVRRIPGPPGPRGAE-GDSGV--QGG-----PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSESRHPGP-GSFGRGGSLGLGGGGGM-----GPREAEPGELGIALRGGGAADPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLRHDPGRCAQCPAGPMGPPGPRGPPGVPGITGAPG-----LDGIPGRHGTPGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DP----TSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAK 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
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                                     unassigned
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ilarity 25.8%;
Conservative 2:
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                                     collagens
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  Score 140;
                                                                                                                                                                                                                                                                          November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270
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  DB
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  Length 304;
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                                                                                                                                                                                                                                                                                                                                    21-Jan-2000
                                                                                                                                                          CESP: F52B11.4
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Query Match

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A; Molecule type: DNA
A; Residues: 561-647; 'G', 649-666 <AP2>
A; Cross references: EMBL:XS8879; NID:g30013; PIDN:CAA41686.1; PID:g30014
A; Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E
Biochem. J. 280, 617-623, 1991
Biochem. J. 280, 617-623, 1991
A; Tele: The human collagen X gene. Complete primary translated sequence and
A; Reference number: S18249; MJD:92109659; PMID:1764025
A; Accession: S18249
A; Cross-reference: S18249; MID:92109659; PMID:1764025
A; Cross-reference: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095
A; Cross-reference: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30094
A; Cross-reference: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30094
A; Cross-reference: EMBL:X6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, March 1992
A;Reference number: $30085
A;Accession: $30086
A;Molecule type: DNA
A;Residues: 'TIPPYGMYCWVCLL', 52-680 <APT>
A;Cross-references: EMBL:X65120; NID:g23129
A;Cross-references: EMBL:X65120; NID:g23129
A;Note: the initial difference is probably due to translation
A;Apte, S.; Mattei, M.G.; Olsen, B.R.
FBBS Lett. 282, 393-396, 1991
FBBS Lett. 282, 393-396, 1991
A;Molecule type: mRNA
A;Residues: $47.656 <RE2>
A;Residues: $47.656 <RE2>
A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796
A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796
A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014)
A;Note: sequence extracted from NCBIP: Super, M.; Evans, G.; Grant, A;Title: Amino acid substitutions of conserved residues in the carboxyl-terminal dom A;Title: Amino acid substitutions of conserved residues in the carboxyl-terminal dom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text change 22-Jun-1999
C;Accession: S26.96; S30.86; S15826; S18249; A43901; I51870; S21856
C;Accession: S26.96; S30.86; S15826; S18249; A43901; I51870; S21856
R;Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.; Bertling, FEBS Lett. 311, 305-310, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FBBS Lett. 282, 393-396, 1991
A;Title: Cloning of human alpha-1(X) collagen DNA and localization A;Reference number: S15826; MUID:91243838; PMID:2037056
A;Accession: S15826
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N;Alternate names: procollagen alpha 1(X) chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 26.8 Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVAGAAG-
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5; Mismatches 87;
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         the carboxyl-terminal domain
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                                                                                                 G.; Grant,
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F;1-18/Domain: signal sequence #status predicted <SIG> F;1-680/Product: collagen alpha 1(X) chain #status predicted <MAT> F;19-56/Domain: simino-terminal nonhelical #status predicted <NC2> F;57-519/Region: interrupted helical #status predicted <NC2> F;57-680/Domain: amino-terminal nonhelical #status predicted <NC2>
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 520-597,'D',599-680 <WAL>
A;Cross-references: GB:S68531; NID:g545180; PIDN:AAC60615.1; PID:g545181
A;Cross-references: GB:S68531; NID:g545180; PIDN:AAC60615.1; PID:g545181
A;Note: mutant sequence from patient with metaphyseal chondrodysplasia type Schmid
A;Note: a second mutant sequence with 614-Pro is also described
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit ed and subsequently O-glycosylated.
                                                                                                                                                                                                        C;Accession: B44984
R;Shamansky, L.M.; Pratt, D.; Boisvenue, R.J.; Cox, G.N.
Mol. Biochem, Parasitol. 37, 73-86, 1989
A;Title: Cuticle collagen genes of Haemonchus contortus
A;Reference number: A44984; MUID:90136718; PMID:2615789
A;Accession: B44984
                                                                                                                                                                                                                                                                                                                          collagen - nematode (Haemonchus contortus) (fragment)
C;Species: Haemonchus contortus
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be important for skeletogenesis C;Superfamily: collagen alpha 1(VIII) chain; complement Ciq C;Keywords: colled coll; extracellular matrix; glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 52/1
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A;Accession: I51870
                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-210 <SHA>
A;Cross-references: GB:J04671;
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Best I
                                                                                                               Superfamily: unassigned
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    176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDP--TSNATSRGAEGPLPPPSMPAVAGAAG 233
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                                                            Local
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Pred. No. 0.023;
                                                          Score 139.5; DB 2; Pred. No. 0.0072;
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3; Mismatches
                                       Mismatches
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collagen alpha 1(XI) chain - bovine (fragments) (;Specises: Bos primigenius taurus (cattle) (cattle) (chate: 22-Nov-1993 #sequence revision 23-Mar-1995 #text change 02-Jul-1998 (;Accession: S18251; C46662; Ā56978; S65884; D46662; E46662; F46662; G46662; R;Brown, K.E.; Lawrence, R.; Sonenshein, G.E. J. Biol. Chem. 266, 23268-23273, 1991 J. Biol. Chem. 266, 23268-23273, 1991 A;Reference number: S18251; MUID:92078200; PMID:1744123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: JE0291
R;Totaro, A.; Grifa, A.; Carella, M.; Rommens, J.M.; Valentino, R;Totaro, A.; Grifa, A.; Carella, M.; Rommens, J.M.; Valentino, Biochem. Biophys. Res. Commun. 250, 555-557, 1998
A;Title: Cloning of a new gene (FB19) within HLA class I region.
A;Reference number: JE0291; MUID:99003493; PMID:9784381
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A; Residues: 1-940 < TOT>
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                                                                                                                                                                                                                                                                                                                                             816 H---EGP
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Pred. No. 0
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                              collagen mRNAs in bovine
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                                                                                                                          H46662;
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A, Molecule type: protein
A, Molecule type: protein
A; Residues: 347-354;356-363;586-600;912-924;925-961;962-998;999-1024 <MAY>
A; Experimental source: vitreous humor
A; Note: sequence modified after extraction from NCBI backbone
R; Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A; Title: Structural analysts of cross-linking domains in cartilage type XI collagen. Ins
A; Reference number: A56978; MUID:95370194; PMID:7642541
A; Reference number: A56978; MUID:95370194; PMID:7642541
A; Residues: 206-229 <MUA>,
R; Nivibizi, C; Eyre, D.R.
Eux. J. Biochem. 224, 943-950, 1994
A; Title: Structural characteristics of cross-linking sites in type V collagen of bone. A; Reference number: 348210; MUID:95010086; PMID:7925418
A; Accession: S65864
A; Molecule type: protein
A; Residues: 'X', 273-298 <NIY>
C; Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
C; Keywords: hydroxyproline
F;211,223/Modified site: 4-hydroxyproline (Pro) #status experimental
A24450

collagen alpha 2(VIII) chain - bovine (fragment)

N;Alternate names: 50K-A collagen (VIII), Descemet's

C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Mar-1988 #sequence_revision 05-Apr-1995 #t

C;Accession: S12898; A24450

C;Accession: S12898; R; Korsching, E.; Kuehn, K.; Rau

R;Mann, K.; Jander, R.; Korsching, E.; Kuehn, K.; Rau
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R; Mayne, R.; Brewton, R.G.; Mayne, P.M.; Ba
J. Biol. Chem. 268, 9381-9386, 1993
A; Title: Isolation and characterization of
A; Reference number: A46662; MUID:93252802;
A; Accession: C46662
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A;Molecule type: mRNA
A;Residues: 1-911 <BR
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Matches 90
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                                                                                                                                                                                                                                             GPPGPLGPPGL
                                                                                                                                                                                                                                                                                      GP--PQSPPNI 336
                                                                                                                                                                                                                                                                                                                              FPGPPGPIGLQGLPG-
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                                                                                                                                                                                                                                                                                                                                                                                                                ---- LPGPAGPAGS----- PGEDGDKGEIGEPGQKGSKGDKEGQQGMFGQGDEGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GHPGPPGPPGEQG-----LPGAAGKEGAKGDPGPQGVSGKDGP-
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Conservative 1
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Pred. No. 0.043;
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                           Rauterberg,
                                                               #text_change
                                                                                                                 membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PGSFGRG-----
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                                                                      03-May-1996
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173 GGAVPRKPVSEMPMERDRGAAHSLEPGKENL-----PGD--PTSNATSRGAEGPLPPPS 224

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A; Molecule type: protein
A; Residues: 1-469 (MAN>
R; Kapoor, R.; Bornstein, P.; S
Biochemistry 25, 3930-3937, 11
A; Title: Type VIII collagen f:
A; Reference number: A90507; M
                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence revision 28-May-1992 #text_change 13-Aug-1999
C;Accession: A41182; A44885
R;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
J. Biol. Chem. 266, 16862-16869, 1991
A;Title: Mouse type II collagengene. Complete nucleotide sequence, exon st.
A;Reference number: A41182; MUID:91358489; PMID:1885613
A;Accession: A41182
                                                                       A;Cross-references: GB:S63190; NID:g234368; PIDN:AAB19627.1; PID:g234369
A;Note: sequence extracted from NCBI backbone (NCBIN:63190, NCBID:63192)
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trin
F;1191-1419/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                              A;Cross-references: GB:M65161
R;Cheah, K.S.; Lau, E.T.; Au, P.K.; Tam, P.P.
Development 111, 945-953, 1991
A;Title: Expression of the mouse alpha 1(II) collagen gene
A;Reference number: A44885; MUID:91347939; PMID:1879363
A;Accession: A44885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 1-24 <KAP>
C;Superfamily: collagen alpha 1(VIII) chain; complement
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A; Residues: 1-28 < CHE>
                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1419 < MET>
                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; not compared with
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Matches
                Query Match
Best Local &
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                7.5%; Score 138.5; DB 2; 30.1%; Pred. No. 0.066;
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MUID:86296625; PMID:3527259
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Pred. No. 0.0
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A;Accession:
A;Molecule ty
A;Residues: 1
                                                                                                                                      collagen alpha 2(XI) chain precursor - human (fragment)
N;Alternate names: procollagen alpha 2(XI) chain
N;Contains: proline/arginine-rich protein (PARP)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C;Accession: S34790; A32645
R;Zhidkova, N.I.; Brewton, R.G.; Mayne, R.
FEBS Lett. 336, 25-28, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 16-C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 16-C;Date: 28-May-1992 #sequence, E.; Vuorio, E.
R;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
J. Biol. Chem. 266, 16862-16869, 1991
J. Biol. Chem. 266, 16862-16869, 1991
J. Fittle: Mouse type II collagen gene. Complete nucleotide sequence, A;Title: Mouse type II collagen gene.
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A; Residues: 1-1487 AMET>
A; Cross-references: GB.M65161
C; Superfamily: collagen alpha
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                                                                     A; Reference number: S34790; MUID: 93314796; PMID: 8325374
                                                                                                                   A; Title: Molecular cloning of PARP (proline/arginine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; not compared with conceptual translation
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Pred. No. 0.0
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                                                                                                                      human
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                                                                                                                   cartilage
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F;429-431/Region: cell attachment (R-G-D) motif
F;429-431/Region: cell attachment (R-G-D) motif
F;429-449/Region: cell attachment (R-G-D) motif
F;1257-1259/Region: cell attachment (R-G-D) motif
F;1257-1259/Region: carboxyl-terminal nonhelical telopeptide
F;1357-1380/Region: carboxyl-terminal propeptide (fragment) #status predicted x;1403-1546/Domain: carboxyl-terminal propeptide (fragment) #status at x;1403-1546/Domain: carboxyl-terminal propeptide (fragment) #status at x;1403-1546/Domain: carboxyl-terminal propeptide
F;1409-163,1511-1545/Disulfide bonds: #status predicted
F;190-163,1511-1545/Disulfide bonds: #status predicted
F;1919/Rodified site: allysine (Lys) #status predicted
F;1919/Rodified site: carbohydrate (Lys) (covalent) #status predicted
F;219/Rodified site: carbohydrate (Lys) (covalent) #status experimental
F;920/Rodified site: 4-hydroxyproline (Pro) #status experimental
F;942,1023,1299/Modified site: 5-hydroxylysine (Lys) #status experimental
F;1427,1433,1450,1459/Disulfide bonds: interchain #status predicted
F;1427,1433,1450,1459/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: structural component of extracellular fibrous polymer associated with ce A;Note: may play a role in controlling the lateral growth of collagen II fibrils C;Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol F;1-254/Domain: non-collagenous (fragment) #status predicted <NC3> F;1-187/Product: prolline/arginine-rich PARP protein (fragment) #status predicted <PARP> F;255-305/Domain: collagenous, triple helix #status predicted <COL2> F;206-342/Domain: non-collagenous #status predicted <NC2> F;306-342/Domain: non-collagenous #status predicted <NC2> F;306-342/Domain: non-collagenous #status predicted <NC2> F;306-342/Domain: non-collagenous #status predicted <NC2>
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A;Residues: 586-1546 <KIM>
A;Residues: 586-1546 <KIM>
A;Residues: 586-1546 <KIM>
A;Residues: 586-1546 <KIM>
A;Residues: GB:044974; NID:g180714; PIDN:AAA52034.1; PID:g180715
A;Note: parts of this sequence were determined by protein sequencing
C;Comment: Prolines and lysines at the third position of the tripeptide:
ed and subsequently O-glycosylated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 6p21.3-6p21.3
A;Map position: 6p21.3-6p21.3
A;Introns: 1302/3; 1330/3; 1332/3; 1350/3; 1440/1; 1477/3
A;Note: the list of introns is incomplete
C;Complex: type XI collagen may be a heterotrimer of two alpha 1(XI) chains (see PIR:CG C;Complex: type XI collagen may be a heterotrimer of two alpha 1(XI) chains (see PIR:CGHUGC), initially linked by disulfide bonds among their carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:L18987; NID:g306439; PIDN:AAA35498.1; PID:g306440 R;Kimura, T.; Cheah, K.S.E.; Chan, S.D.H.; Lui, V.C.H.; Mattei, M.G.; van der Rest J. Biol. Chem. 264, 13910-13916, 1999 A;Title: The human alpha2(XI) collagen (COL11A2) chain. Molecular cloning of cDNA A;Reference number: A32645; MUID:89340485; PMID:2760050 A;Accession: A32645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: COL11A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
                                                                          310 HYEK-VSGDYGHPVYIVQDGPP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
KGEKGVQGPPGHP----GPP 1353
                                                                                                                                                                                                                                                                                                                                                                                                        GDPTS-----NATSR-GAEGPLPPPSMPAVAGAAGGLALL----LLGVAGAGGAMCWR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSEGROGG----KGAK-----GDPGAIGAPGKTGPVGP-----AGPAGKPGPDGLR 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRK--PVSEMPMBRDRGAAHSLEPGKENLP
                                                                                                                                                              -EQGEKGDRGLÞGÞQGSÞGQKGEMGIÞGASGÞIGÞ-GGÞÞGLÞGÞAGÞKGAKGATGÞGGÞ
                                                                                                                                                                                                                                                                                                                        GLPGSVGQQGRPGATGQAGPPGPVGPPGLPGLRGDAGAKGEKGHPGLIGLIGPPG-----
                                                                                                                                                                                                                                             RRRAKPSESRHPGP-GSFGRGGSLGL-GGGGGMGPREAEPGELGIA-LRGGGAADPPFCP
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31.7%; Pre
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Pred. No. 0.072;
8; Mismatches
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Search completed: February Job time: 36.805 secs

11, 2003,

12:06:08

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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
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seq length: 2000000000
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* (cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

* (cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

* (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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   GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
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US-09-925-297-639
US-09-862-179A-15
US-09-862-179A-16
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Sequence 4, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 9, Appli
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Sequence 10, Appli
Sequence 10, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 13, Appl
Sequence 48257, A
Sequence 48257, A
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
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Sequence 12, Appl
Sequence 13, Appl
Sequence 12, Appl
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09-978-189-61	9-832A-6	09-978-192A-6	-978-	-978-295A-6	US-09-925-302-689	US-09-919-497-56	US-09-738-973-187	-187	US-09-925-299-979	US-09-823-240-10	US-10-001-887-108	US-09-862-179A-2	US-09-925-301-1225	US-10-138-787~9	10-176-921-28	10-176-918-28	10-175-746-28	10-140-470-28	10-123-904-28	US-10-121-049-288	10-028-072-2	10-001-054-4	10-138-787-1	08-578-684-	10-138-787-	10-138-787-	S-09-904-95	US-09-925-297-510	10-138-787	CO-03-361-2
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ALIGNMENTS

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US-10-021-121-4
Sequence 4, Application US/10021121
Patent No. US20020142444A1
GENERAL INFORMATION:
APPLICANT: CATAS, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: Callitornia
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER SEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER SEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER IN PC COMPATIBLE
OPERATING SYSTEM, PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
FILING DATE: 106-Dec-2001
CLASSIFICATION NUMBER: US/08/635,130
FILING DATE: 19-MAX-1996
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHAA, PhD., Timothy E.
REGISTRATION NUMBER: 15,700
REFERENCE/DOCKET NUMBER: 56,700
REFERENCE/DOCKET NUMBER: 56,700
REFERENCE/DOCKET NUMBER: 56,700
REFERENCE/DOCKET NUMBER: TOTCHAA, PhD., Timothy E.
REGISTRATION INFORMATION:
TELEFAX: 650/952-98674
TELEFAX: 650/952-98674
TELEFAX: 650/952-98674
INFORMATION TORNATION:
LENGTH: 340 amino acids
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APPLICANT: Moliand, Sacha
APPLICANT: Mosmalu, Geraldine
APPLICANT: Mosmalu, Geraldine
APPLICANT: Mosmalu, Geraldine
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT APPLICATION NUMBER: US/99/214,631
PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1997-07-05
INUMBER OF SEQ ID NOS: 13
SOSTWARE: Patentin Ver. 2.0
TYPE: PRT
CREATER HOME SERVICES
TYPE: PRT
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TYPE: PRT
CREATER HOME SERVICES
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TYPE: Amino Acid
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TOPOLOGY: Linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                          Query Match
Best Local Similarity 99.7
Conservative
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Best Local Similarity 100.
Matches 340; Conservative
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      LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY
                                          LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLITCDRPDLDLRFTIKFQEY 120
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                                                                                                                                                         99.8%; Score 1846; DB 9; Length 340; 99.7%; Pred. No. 1.7e-125; rative 1; Mismatches 0; Indels
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Pred. No. 8.7e-126;
0; Mismatches 0;
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RESULT 3
US-10-021-121-2
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                                                                                                                                                                                                                             Matches 338;
                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION NUMBER: US/00/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION NUMBER: US/08/635,130
FRICR APPLICATION NUMBER: US/08/635,130
FRICR APPLICATION NUMBER: US/08/635,130
FRICR APPLICATION NUMBER: US/08/635,130
RESERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHYNES SEC/082-0887
TELEPHYNES SEC/082-0887
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                                                                                                                                                                               1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
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                                           LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPHLLLTCDRPDLDLRFTIKFQEY
                                                                        LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
                                                                                                                                  MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYMNSANKRFQAEGGYVLYPQIGDRLDL 60
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ZIP: 94080
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                                                                                                                                                                                                                      99.5%; Score 1841; DB 12; ilarity 100.0%; Pred. No. 5.3e-125; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                      Length 455;
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US-10-021-121-9
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPacin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/021,121

FILING DATE: 06-Dec-2001

CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/635,130

FILING DATE: 19-Mar-1996

APPLICATION NUMBER: US/08/635,130

FILING DATE: 19-Mar-1996

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 91001

TELEPONNE: 650/225-8674

TELEPAX: 650/952-9811

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 SANIOR SCIES
                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 145; Conserv
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Patent No. US20020142444A1
GENERAL INFORMATION:
119
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TITLE OF INVENTION: A2-1 Neurotrophic Factor
                                                                                                                                                                          PGGVRVGALLLLGVLGLVSGL-----SLEPVYMNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                                                          CPRAEAGRP----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
                  PNLMGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                                                                                                              CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
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PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
                                                                                                                                                     PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
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                                                                                                                                                                                                                                                                                                                                              LENGTH: 346 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                              Score 632; DB 12;
Pred. No. 2.1e-38;
8; Mismatches 116;
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                                                                                                                                                                                                                                                                 Length 346;
                                                                                                                                                                                                                                  Indels 58;
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; LENGTH: 333
; TYPE: PRT
; ORGANISM: homo :
US-09-754-105-2
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CURRENT FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: 09/329,531
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09754105
Patent No. US20010009768A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cerretti, Douglas
APPLICANT: Reddy, Pranhitha
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5
FILE REFERENCE: 28232
 304
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                                                                                                                                                                                                                                                                                                                                         GVLMVLCRTAISKSIVLBPIYMNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                 YEKVSGDYGHPYYIVQDGPPQSPPNIYYKV 340
                                                                KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIPLR---TADSVFCPH
                                                                                                    WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGPREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                      GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                                                                                                                          DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                               PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
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                                                                                                                                       GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL
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US-09-978-339-2

Sequence 2, Application US/09978339 Patent No. US20020103358A1 GENERAL INFORMATION:

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TOPOLOGY: linear;
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-978-339-2
WS-10-021-121-10
US-10-021-121-10
; Sequence 10, Application US/10021121
; Patent No. US20020142444A1
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Best Local Similarity
Matches 135; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 15-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/271,948
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2823
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reddy, Pranhitha
TITLE OF INVENTION: NO. US20020103358A1el Cytokine Designated Lerk-5
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                             YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                       WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                                                                                                                                                                                                                                                                                                                       GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVLMVLCRTAISKSIVLEPIYMNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
                                                                                                                   YEKVSGDYGHPVYÍVQEMPPQSPANIYYKV 333
                                                                                                                                                                                                   KYRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH
                                                                                                                                                                                                                                                                                  GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFÄGIÄSGCIIFIVIIITLVVLLL
                                                                                                                                                                                                                                                                                                                                                               DYYTTSTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
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OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version
ENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
COUNTRY: US
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STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 333 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 587-04
TELEFAX: (206) 233-0644
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Pred. No. 3.1e-38;
52; Mismatches 130;
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GENERAL INFORMATION:

APPLICANT: Caras, Ingrid W
ITTLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CTMY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-021-121-10
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PRILING DATE: 19-Max-1996
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 91001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEPHONE: 650/225-8674
TELEPHONE: 650/225-8674
TELEPHONE: 650/225-861
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 135; Conservative
  304
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WilhPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
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YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333
                                                                                  KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIPLR---TADSVFCPH
                                                                                                                           WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGGGGFREAEPGELGIALRGGGAADPPFCPH
                                                                                                                                                                                                                                                                                   DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
                                                                                                                                                                                                                                                                                                                                              GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
                                                                                                                                                                                                                                                                                                                                                                                     PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                           YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
                                                                                                                                                                       GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFÅGIÅSGCIIFIVIIITLVVLLL
                                                                                                                                                                                                              GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                                                                                                                                                                                                                                                            DYYIISTSNGSLEGIDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                   GVIMVICRTAISKSIVLEÞIYMNSSNSKFLÞGQGLVLÝÞQÍGDKLDIICÞKV---DSKTV 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 629.5; DB 12;
Pred. No. 3.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT 8 US-10-138-787-4

Sequence 4, Application US/10138787 Patent No. US20020172984A1 GENERAL INFORMATION: APPLICANT: Holland, Sacha

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GENERAL INFORMATION:

APPLICANT: Holland, Sacha

APPLICANT: Mbamalu, Geraldine

APPLICANT: Mbamalu, Geraldine

APPLICANT: Pawson, Tony

TITLE OF INVENTION: DIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED

TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

TITLE OF INVENTION: TYROSINE KINASES

FILE REFERENCE: 11757_23USWO

CURRENT APPLICATION NUMBER: US/10/138,787

CURRENT APPLICATION NUMBER: US/09/214,631

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: BCT/CA97/00473

PRIOR APPLICATION NUMBER: BCT/CA97/00473

PRIOR APPLICATION NUMBER: 60/021,272

PRIOR FILING DATE: 1999-07-04

PRIOR FILING DATE: 1999-07-05

PRIOR FILING DATE: 1996-07-05

PRIOR FILING DATE: 1996-07-05

PRIOR FILING DATE: 1996-07-05

PRIOR FILING DATE: 1996-07-05

PRIOR FILING DATE: 1998-07-05
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APPLICANT: Pawson, Tony
ITILE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
ITILE OF INVENTION: BY TRANSMEWBRANE LIGANDS FOR ELK-RELATED RECEPTOR
ITILE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT AFPLICATION NUMBER: US/10/138,787
CURRENT AFPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
PRIOR FILING DATE: 1996-07-05
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; ORGANISM: Homo
US-10-138-787-4
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33.6%; Score 622.5; DB 9;
Best Local Similarity 40.9%; Pred. No. 9.7e-38;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
SOFTWARE: PatentIn Ver.
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APPLICANT: Mamalu, Geraldine
APPLICANT: Mamalu, Geraldine
APPLICANT: Mamalu, Geraldine
APPLICANT: Mamalu, Geraldine
APPLICANT: Pawson, Tony
ITILE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
ITILE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT FILING DATE: 1052-05-03
PRIOR APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 199-03-12
PRIOR APPLICATION NUMBER: POT/CA97/00473
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: BO/021,272
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 89
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                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-13
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US-10-138-787-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/10138787 Patent No. US20020172984A1 GENERAL INFORMATION:
                                                                    Query Match 20.0%;
Best Local Similarity 100.0%;
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Best Local Similarity
Matches 142; Conserv
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252 RRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 STIASPKGGSGTAGTEPSDIIIPL---FTTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
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                                                            89;
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                                                                          26.9%; Score 498; DB 9; 1
100.0%; Pred. No. 1.9e-29;
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                                                            0; Mismatches
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US-09-862-179A-17
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US-09-864-761-48262
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                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: DET/US01/00666
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
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CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48262, Applicatio Patent No. US20020048763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.9%; Score 498; DB 10; Best Local Similarity 100.0%; Pred. No. 1.9e-29; Matches 89; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Penn, Sharron
APPLICANT: Rank, David F
APPLICANT: Hanzel, David
APPLICANT: Chen, Wensher
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TITLE OF INVENTION: PETTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS
TITLE OF INVENTION: AND PDZ DOMAINS
FILE REFERENCE: MTSI-P01-009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lin, Danny APPLICANT: Pawson, Ar
                                                                               PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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                     CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: DS/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR HILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
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Best Local S
Matches 52
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SOFTMARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 48262
LENGTH: 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 48257, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-66-30
PRIOR FILING DATE: 2000-6774,203
PRIOR FILING DATE: 2001-01-29
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Pred. No. 4.1e-14;
5; Mismatches 24
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Length 92;

5

Gaps

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PROBES USEFUL

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GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA105

FILE REFERENCE: PA105

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: ECT/US00/05989

PRIOR FILING DATE: 2000-03-08

PRIOR PAPLICATION NUMBER: 60/124,270

PRIOR PAPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 639

LENGTH: 106

TYPE: PRT

ORGANISM: Homo sapiens

US-09-925-297-639
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US-09-925-297-639
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Best Local
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSFGRGGSLGL----GGGGGMGPREAEPGELGIALRGGGAADPFFCPHYEKVSGDYGHPV 322
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                                                                                                                                                                                                                                                                                                                           and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 = 1.4
LUE 2.00e-26
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Sequence 15, Application US/09862179A

Patent NO. US20020147306A1

PATENTIAL INFORMATION:
APPLICANT: Lin, Danny
APPLICANT: Lin, Danny
ITITLE OF INVENTION: PEPTIDES THAT MODULATE THE INT
ITITLE OF INVENTION: AND PDZ DOWAINS
FILE REFERENCE: MTG1-P01-009

CURRENT APPLICATION NUMBER: US/09/862,179A

CURRENT FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin version 3.1

SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 199-03-12
PRIOR FILING DATE: 199-03-12
PRIOR FILING DATE: 199-07/CA97/00473
PRIOR FILING DATE: 199-07-07
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-10-138-787-11
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US-09-862-179A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: Mbamalu, Geraldine
APPLICANT: PAWSON, TONY
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULA
TITLE OF INVENTION: BY TRANSMEWSRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
TYPE: PRT
ORGANISM: Homo sapiens
                                        ENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 LALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGL----GGGGGMGPREAEP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 RRRRAKPSESRHPGPGSFGRGGSLGL----GGGGGMGPREAEPGELGIALRGGGAADPPF 307
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                                                                                                                                                                                                                                                                                                                                                                                                                              50 CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -RAAALSÍSTLASPKGGSGTAGTÉPSDIIÍPÍR---TTENNY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
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Pred. No. 3.6e-08;
9; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                              82
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US-09-862-179A-16
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                                               US-09-862-179A-16
                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09862179A Patent No. US20020147306A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 38; Conservat
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SEQ ID NO 12
LENGTH: 82
TYPE: PRT
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APPLICANT: Holland, Sacha
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Best Local Similarity 47.3
Matches 44; Conservative
Query Match
                                                                                                                                  SOFTWARE: PatentIn version 3.1 SEQ ID NO 16
                                                                                                                                                                          APPLICANT: Lin, Danny
APPLICANT: Pawson, Anthony
TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B
TITLE OF INVENTION: AND PDZ DOMAINS
FILE REFERENCE: MTSI-P01-009
CURRENT FILING DATE: 2001-05-21
NUMBER: OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PAWSON, TONY
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757,23USWO
CURRENT FILLING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/10/138,787
CURRENT FILLING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR FILING DATE: 1996-07-05
PRIOR PILING DATE: 1996-07-05
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR PILING DATE: 1996-07-05
NUMBER: 0F SEQ ID NOS: 13
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                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                               LENGTH: 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%; Score 200.5; DB 9; Length 82; 71.7%; Pred. No. 3.9e-08; tive 4; Mismatches 8; Indels
  10.8%;
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Pred. No. 3.6e-08;
    Score 200.5;
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    10;
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  Length 82;
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                                                                                                                                                                                                                                                                                                 CLASS EPHRINS
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: S

US-09-904-934-2
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US-09-904-954-2
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Patent No. US20020010325A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 AEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
                                       118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/9994,954
FILING DATE: 12-Jul-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-193
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-193
ATTORNEY/AGENT INFORMATION:
127 ORYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG---
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                                                                             68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126
                                                                                                                  65 ARPPGPHSSP----NYEFYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
                                                                                                                                                            24 GPG-----GALG----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67
                                                                                                                                                                                                  7 GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHA: (206) 587-0430
TELEFFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CERRETTI, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BECKMANN, M.
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                              QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVF 177
                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: SEESE, KATHRYN A
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                  9.7%;
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                                                                                                                                                                                                                                                   24;
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                                                                                                                                                                                                                                                Score 179; DB 10;
Pred. No. 4.4e-06;
84; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.
THAT BINDS THE CELL SURFACE
                                                                                                                                                                                                                                                                                                                                                        N
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                                                                                                                                                                                                                                                                                        Length 238;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                   60;
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                                                                                                                                                                                                                                                   Gaps
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LENGTH: 209 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECUL TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-921-984-2
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US-09-921-984-2
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                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 227-5; INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223
                                                                                                                     145 REGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 RKPVSEMP-----PGKENLP 204
175 EAPEPIFTSNSSCSGLGG 192
                                    205 GDP----TSNATSRGAEG 218
                                                                                                                                                                94 GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 151
                                                                                                                                                                                                     88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
                                                                                                                                                                                                                                              35 VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93
                                                                                                                                                                                                                                                                                     33 VYWNSANKRFOAE-----GGYVLYPOIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/921,984
FILING DATE: 31-Ju1-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/308,814
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Flanagan, John G.
APPLICANT: Flanagan, John G.
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011
TELECOMMUNICATION INFORMATION:
TELEPHONE; (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(txt)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                ----PNLVDRPCLR--LKVYVR
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83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 227-74
TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TY: Boston
                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                             9.5%;
                                                                                                                                                                                                                                                                                                                          Score 176; DB 9;
Pred. No. 6.2e-06;
9; Mismatches 69
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                                                                                                                                                                                                                                                                                                                                                                 Length 209;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                          52; Gaps
                                                                                PINETLY 174
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RESULT

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Sequence 7, Application US/10138787

Patent No. US20020172984A1

GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
TITLE OF INVENTION: DIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEWBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: DS/09/214,631
PRIOR APPLICATION NUMBER: DS/09/214,631
PRIOR APPLICATION NUMBER: DS/07/0473
PRIOR APPLICATION NUMBER: DS/07/0473
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1995-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                     APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEG ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 510
LENGTH: 218
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-7
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                                                                                                   ; ORGANISM: Homo sapiens
US-09-925-297-510
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US-09-925-297-510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.4%; Score 174.5; DB 9; Best Local Similarity 27.4%; Pred. No. 9e-06; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 510, Application US/09925297 Patent No. US20020081659A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 TMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 -----PGKENLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 ÉFHAGHEYYYİSTPTHNLH------WKCLR--MKVFVCCASTSHSG---EKPVPTLPQF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 EFRSHHDYYIIATSDGTREGLESLQGGVÇLTRGWKVLLRVGQSPRGGAVPRKPVSEMP-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 YVLYMVSRNGYRTCNASQGFKRWECNRPHAPH-----SPIKFSEKFQRYSAFSLGY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYNSSGAGPGPGGGAE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 GVLGLVSGLSLEÞVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR----ARPPGPHSSPN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEFYKLYLVG-----GAQGRR----CEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGH 127
  Conservative
                       28.3%;
     30;
                          Score 172.5, DB Pred. No. 1.2e-05
     Mismatches
                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218
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     Indels
                                               Length 218;
     19;
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     Gaps
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; Sequence 4, Application US/09904954
; Patent No. US20020010325A1
; GENERAL INFORMATION:
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                                                                                                                                Query Match
Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                                            TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/240,124
FILING DATE: CURKNOWN
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 320,000
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 FTPFTLGKEFKEGHSYYYISKPIHQHEDR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 YSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 YE---DHSVADAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
    83
                                               20
                                                                                 24 LVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82
                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOPTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/904,954
FILING DATE: 12-Uul-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
ATTREFT: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BECKMANN, M. P.
CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
    LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARPPGPHSSPN--YEFYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGGVRVGALLILGVLGLVSGLSL---EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR
                                               LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGQARAMEFLWAPLLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPH
                                                                                                                                66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: SEATTLE
STATE: WASHINGTON
                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 233-0644
                                                                                                                                   Conservative
                                                                                                                                                  9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR HEK
                                                                                                                                18;
                                                                                                                                Score 169.5; DB 10;
Pred. No. 1.7e-05;
B; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---CLRLKVTVSGKITHSPQAHDNPQE 176
                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version
                                                                                                                                   Indels
                                                                                                                                                                         Length 201;
                                                                                                                                55;
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CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 201
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                            RESULT 25
US-10-138-787-6
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US-10-138-787-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-138-787-8
                                                                                                                                                        Sequence 6, Application US/10138787
Patent No. US20020172984A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10138787 Patent No. US20020172984A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                 APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11157.23USWO
                                                                                                                                                                                                                                                                                                                          156
                                                                                                                                                                                                                                                                                                                                                                      188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 9.1%; Score 169; DB 9;
Local Similarity 29.8%; Pred. No. 1.9e-05;
1es 70; Conservative 19; Mismatches 84
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REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
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                                                                                                                                                                                                                                                                                                                          RKSESAHPV-----
                                                                                                                                                                                                                                                                                                                                                                   RDRGAAHSLEPGKENLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPPEGP--ETFALYMVDWPGYESCQAEGPRGYKRWVCSLPFGHVQFSEKIORFTPFSLGF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPHSSPNYEFYKLYLVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLITVLWAAFLGSPLRGGSSLRHVVYWNSSNPR-SLRGDAVVELGLNDYLDIVCPHYEGP 64
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                                                                                                                                                                                                                                                                                                                          -GSPGESGTSGWRGGDTPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
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; ORGANISM: Mus musculus
US-10-138-787-6
US-08-578-684-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
PRIOR FILING DATE: 1996-07-05
PRIOR FILING DATE: 1996-07-05
PRIOR FILING DATE: 1996-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08578684 Patent No. US20020137126A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 42; Conserv
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SEQ ID NO 6
LENGTH: 209
                                                                                                                                                                                           APPLICATION NUMBER: 08/330128
PRILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA: 08/486449
APPLICATION NUMBER: 08/486449
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TORCHIA, PhD: Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0920P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -08-578-684-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb fl.

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WILPATION (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/578,684
                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acid
                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1 DIA CITY: South San
                                      LENGTH: 228 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 GHASCDHRORGEKRWECNRPAAPGGPLKFSEKFOLFTPESLGFEFPPGHEYYYISAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 VYWNRSNPRFOVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 YYWNSANKRFOAE----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
                                                                                                                                                     TELEPHONE:
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                     IOPOLOGY:
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1 DNA Way
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                   Linear
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Sequence 10, Application US/10138787

Patent No. US20020172984A1

GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
TITLE OF INVENTION: DIGOMERIZED RECEPTORS WHICH
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR
TITLE OF INVENTION: TYROSINE KINASES
US-10-001-054-48
, Sequence 48, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-10
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
SEQ ID NO 10
LENGTH: 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 11757.23USWO
                                                                                                                                                           124 HSYYYISKPIHQHEDR---
                                                                                                                                                                                                     133 HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 PADDTV---HESAEPSRG-ENAAQTPRIPSRL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE 197
                                                                                                                                                                                                                                                      64 MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 123
                                                                                                                                                                                                                                                                                                    76
                                                                                                                                                                                                                                                                                                                                                                                         18 LIGVIGIVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 9.0%; Score 166; DB 9; 1
Local Similarity 27.5%; Pred. No. 3.2e-05;
es 46; Conservative 31; Mismatches 74;
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                                                                                                                                                                                                                                                                                                 YEFYKLYLVGGAQGRRCBAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHTSKGFKRWECNRPHSPN-----GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS
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                                                                                                                                                                                                                                                                                                                                                LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSVADAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 9.1%;
l Similarity 28.8%;
65; Conservative 29
                                                                                                                                                                ----CLRLKVTVSGKITHSPQAHVNPQE 16:
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; Pred. No. 2.8e-05; 
29; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHICH AFFECT PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 228;
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APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
TITLE OF INVENTION: CELL GROWTH
FILE REPERENCE: 93094R1PCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
                                                             PRIOR 
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
DR FILING DATE: 1999-06-22

DR APPLICATION NUMBER: 60/141037

DR FILING DATE: 1999-06-23

DR APPLICATION NUMBER: 60/144758

DR FILING DATE: 1999-07-20

DR APPLICATION NUMBER: 60/142506

DR APPLICATION NUMBER: 60/170262

DR APPLICATION NUMBER: 60/170262

DR FILING DATE: 1999-12-09
                                                                                                                                                                                                                                                                                                                                                                                            OR FILING DATE: 1999-01-12

OR APPLICATION NUMBER: 60/115558

OR APPLICATION NUMBER: 60/116533

OR FILING DATE: 1999-01-20

OR APPLICATION NUMBER: 60/123618
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R FILING DATE: 1998-12
R APPLICATION NUMBER: 6
R APPLICATION NUMBER: 6
R APPLICATION NUMBER: 6
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R APPLICATION NUMBER: (
R FILING DATE: 1998-06.
R FILING DATE: 1998-06.
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FILING DATE: 1998-0.
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                 FILING DATE: 1999-03-10
APPLICATION NUMBER: 60/1
FILING DATE: 1999-04-07
APPLICATION NUMBER: 60/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 1998-0: APPLICATION NUMBER:
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APPLICATION I
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Gurney, Austin
Hebert, Carolyn
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IOR FILING DATE: 2001-08-13
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DR FILING DATE: 2001-08-06

DR APPLICATION NUMBER: 099327796

DR FILING DATE: 2001-08-06

DR APPLICATION NUMBER: 099329404
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APPLICATION NUMBER: 60/209832
FILING DATE: 2000-06-05
APPLICATION NUMBER: 60/232887
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APPLICATION NUMBER: 09/866034
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APPLICATION NUMBER: 09/802706
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APPLICATION NUMBER: 09/
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2000-02-18

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; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo S
US-10-001-054-48
                                                                                                  RESULT 29
US-10-028-072-288
; Sequence 288, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 46; Conserv
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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OR APPLICATION NUMBER: PCT/US00/14941
OR FILING DATE: 2000-05-30
OR APPLICATION NUMBER: PCT/US00/15264
OR FILING DATE: 2000-06-02
OR APPLICATION NUMBER: PCT/US00/22031
OR APPLICATION NUMBER: PCT/US00/23522
OR APPLICATION NUMBER: PCT/US00/23522
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APPLICATION NUMBER: PCT/US01/27099
FILING DATE: 2001-08-29
R OF SEQ ID NOS: 91
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APPLICATION NUMBER: PCT/US01/21066
FILING DATE: 2001-06-29
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APPLICATION NUMBER: PCT/US00/30873
FILING DATE: 2000-11-10
APPLICATION NUMBER: PCT/US00/32678
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FILING DATE: 2000-03-30
APPLICATION NUMBER: PCT/US00/13705
FILING DATE: 2000-05-17
APPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: PCT/US01/17092
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APPLICATION NUMBER: PCT/US00/06884
FILING DATE: 2000-03-15
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APPLICATION NUMBER: PCT/US00/05841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH 133
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27.7%; Pred. No. 4.1e-05;
rative 31; Mismatches 74; Indels
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FILE REFERENCE:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
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PRIOR PILING DATE: 1997-06-18
PRIOR PPLICATION NUMBER: 60/056974
PRIOR PPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/05912
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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OR FILING DATE: 1997-09-24
OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062285
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/06287
OR FILING DATE: 1997-10-17
OR PELICATION NUMBER: 60/062814
OR APPLICATION NUMBER: 60/062814
OR APPLICATION NUMBER: 60/062814
OR APPLICATION NUMBER: 60/062816
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063045
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063082
OR APPLICATION NUMBER: 60/063082
OR APPLICATION NUMBER: 60/063127
OR FILING DATE: 1997-10-31
OR APPLICATION NUMBER: 60/063127
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OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059122
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059184
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059263
OR FILING DATE: 1997-09-18
OR FILING DATE: 1997-09-18
OR APPLICATION NUMBER: 60/063733
OR FILING DATE: 1997-10-29
OR PELICATION UNBER: 60/063735
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063738
OR APPLICATION NUMBER: 60/063755
OR APPLICATION NUMBER: 60/063755
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APPLICATION NUMBER: 60/63329
FILING DATE: 1997-10-27
APPLICATION NUMBER: 60/663550
FILING DATE: 1997-10-28
FILING DATE: 1997-10-28
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FILING DATE: 1997-09-19
APPLICATION NUMBER: 60/059588
FILING DATE: 1997-09-19
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APPLICATION NUMBER: 60/063704
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APPLICATION NUMBER: 60/063561
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Watanabe, Colin
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Stewart, Timothy A.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/64248
OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/064809
OR FILING DATE: 1997-11-07
OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065846
OR FILING DATE: 1997-11-17
OR APPLICATION NUMBER: 60/066364

OR APPLICATION NUMBER: 60/066453
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/066511
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/069212
OR APPLICATION NUMBER: 60/069212
OR FILING DATE: 1997-12-11

FILING DATE: 1997-11-21

APPLICATION NUMBER: 60/069278 FILING DATE: 1997-12-11 APPLICATION NUMBER: 60/069334

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RESULT 30
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OR FILING DATE: 1998-06-24
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OR APPLICATION NUMBER: 60/091360
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091982
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OR FILING DATE: 1998-05-22
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OR APPLICATION NUMBER: 60/088726
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OR APPLICATION NUMBER: 60/089907
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OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085579
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OR APPLICATION NUMBER: 60/085697
OR APPLICATION NUMBER: 60/085704
OR APPLICATION NUMBER: 60/085704
OR APPLICATION NUMBER: 60/085704
OR FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/090445
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                                                                                                                                                                        DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
                                                                                                                                                                                                                                   EQYILYLVEHEBYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGH
                                                                                                                                                                                                                                                                                        EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH:133
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ilarity 27.7%;
Conservative 3
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Pred. No. 4.1e-05;
1; Mismatches 74;
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OR FILING DATE: 1997-12-11
OR APPLICATION NUMBER: 60/069694
OR FILING DATE: 1997-12-16
OR APPLICATION NUMBER: 60/072320
OR FILING DATE: 1998-01-23
OR APPLICATION NUMBER: 60/073612
OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/074096
OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/074092
OR APPLICATION NUMBER: 60/07791
OR FILING DATE: 1998-03-09
OR APPLICATION NUMBER: 60/07791
OR FILING DATE: 1998-03-12
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078910
OR APPLICATION NUMBER: 60/078910
OR APPLICATION NUMBER: 60/079294

PRIOR

OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079663
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OR APPLICATION NUMBER: 60/079728
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/080165
OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/081203

миливек: 60/079728 : 1998-03-27

DR FILING DATE: 1998-04-09
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DR FILING DATE: 1998-04-14
DR APPLICATION NUMBER: 60/081817

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APPLICATION NUMBER: 60/082999
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APPLICATION NUMBER: 60/083322

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FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083545

FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/084627

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1998-05-07

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DR APPLICATION NUMBER: 60/085149
DR FILING DATE: 1998-05-12
DR APPLICATION NUMBER: 60/085323
DR FILING DATE: 1998-05-13
DR APPLICATION NUMBER: 60/085338
DR APPLICATION NUMBER: 60/085338
DR FILING DATE: 1998-05-13

, Sequence 288, Application Publication No. US2003002 GENERAL INFORMATION: GAPPLICANT: Baker, Kevin PAPPLICANT: Beresini, Mau

Application US/10121049 b. US20030022239A1

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US-10-123-904-288
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; ORGANISM: Homo Sapien
US-10-121-049-288
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Best Local Similarity
Matches 46; Conserv
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LENGTH: 204
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CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
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                 CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
                                                APPLICANT: Zhang, Zemin
TITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
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NUMBER OF SEQ ID NOS: 550
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                                                                                                                Tumas, Daniel
Watanabe, Colin K
Wood, William
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Desnoyers, Luc
Filvaroff, Ellen
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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See File Wrapper or Palm
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; Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550 ; SEQ ID NO 288 ; LENGTH: 204 ; TYPE: PRT : ORGANLEM: Homo Sapien US-10-140-470-288
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-288
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SEQ ID NO 288
LENGTH: 204
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Best Local Similarity
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Best Local Similarity 27.7'
Matches 46; Conservative
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
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                                                                    64 EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKBFKEGH 123
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                                                                                                                  EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH 133
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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;; Pred. No. 4.1e-05;
31; Mismatches 74; Indels
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; TYPE: PRT; ORGANISM: Homo Sapien US-10-175-746-288
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Matches
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APPLICANT: Baker, Ke
APPLICANT: Beresin
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Publication No.
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Publication No. US20030027270A1
GENERAL INFORMATION:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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Local Similarity 27.7%;
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            Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
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Filvaroff, Ellen
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                                                                              US-10-176-921-288
                                                                                                                                Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550 SEQ ID NO 288 LENGTH: 204
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 288
LENGTH: 204
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Publication No.
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  Matches
                  Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C182
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C288 CURRENT APPLICATION NUMBER: US/10/176,921 CURRENT FILING DATE: 2002-06-20
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                           ORGANISM: Homo Sapien
                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LIGICCSLAAADRHTVFWNGSNFKFRNE-DYTIHVQLNDYVDXICFHYB---DHSADAAM 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH 133
46;
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Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                             Zhang, Zemin
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Wood, William
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                                                                                                                                                                                                                                                                                                                                                                                                         Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pesnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beresini,Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10176921
  Conservative
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                  8.9%; Score 164.5;
27.7%; Pred. No. 4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
    Mismatches
                    4.1e-05
                                     DB 9;
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CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/99/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR REPLICATION NUMBER: PCT/CA97/00473
PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1996-07-05
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 228
                                                                                                                                                                                                     RESULT 37
US-09-925-301-1225
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; ORGANISM: Homo sapiens
US-10-138-787-9
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US-10-138-787-9
                 Sequence 1225, Application US/09925301
Patent NO. US2002052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/10138787
Patent No. US20020172984A1
GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: TYROSINE XINASES
FILE REFERENCE: 11757.23USWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.7%; Score 160.5; DB 9; Best Local Similarity 28.3%; Pred. No. 8.9e-05;
  PRIOR APPLICATION NUMBER: PCT/US00/05882
                                                                                                                                                                                                                                                                                                 187 PADDTV---HESAEPSRG-ENAAQTPRIPSRL----LAILLFLLA 223
                                                                                                                                                                                                                                                                                                                                                198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 DHTSKGFKRWECNRPHSPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 YYWNSANKREQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG----- 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
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                                                                                                                                                                                                                                                                                                                                             PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                     S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH 133
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                                                                                                                                                                                                                                                                                                                                                                                            -----CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GPLKFSEKFQLFTPFSLGFEFPPGREYFYISS 141
                                                                                          and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 228;
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                                                                                                        RESULT 39
US-10-001-887-108
; Sequence 108, Application US/10001887
; Patent No. US2002015464A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PAWSON, Anthony
TITLE OF INVENTION: APPTIDES THAT MODULATE THE INTERACTION OF
TITLE OF INVENTION: AND PDZ DOMAINS
FILE REFERENCE: WISI-P01-009
CURRENT PILING DATE: 2001-05-21
NUMBER OF SEC ID MOS: 44
SOFTWARE: Patentin version 3.1
SEC ID MO 2
LENGTH: 28
TYPE: PRT
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SEQ ID NO 1225
LENGTH: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.3%; Score 154; DB 10; Best Local Similarity 100.0%; Pred. No. 2.4e-05; Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                   APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
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PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
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OTHER INFORMATION: Xaa=Ala or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC_FEATURE LOCATION: (21)...(21) OTHER INFORMATION: Xaa=Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC FEATURE LOCATION: (20)..(20)
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OTHER INFORMATION: PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                         308 CPHYEKVSGDYGHPVYIVQDGPPQSP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 VSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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Sun,
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  Yongming
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Pred. No. 0.00022;
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                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
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US-09-823-240-10
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                                                                                                                                                                    US-09-823-240-10
                                                                                Query Match
Best Local S
Matches 67
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TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes |
FILE REFERENCE DEX-0269
CURRENT APPLICATION NUMBER: US/10/001,887
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/449,998
PRIOR FILING DATE: 2000-11-20
PRIOR PRIOR DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-22
SPRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
SEQ ID NO 108
LENGTH: 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09823240 Patent No. US20020048813A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.5%; Score 138; DB 9; Length 638; Best Local Similarity 27.9%; Pred. No. 0.011; Matches 68; Conservative 13; Mismatches 79; Indels
                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          APPLICANT: Jurgen Wehland
APPLICANT: Joseph Loureto
ITITLE OF INVENTION: Methods and Products for Regulating Cell
ITITLE OF INVENTION: Mothlity
FILE REFERENCE: MO556/7064 (HGL)
CURRENT APPLICATION NUMBER: US/09/823,240
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 60/194,564
PRIOR APPLICATION NUMBER: 60/194,564
PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Frank B. Gertler APPLICANT: James E.Bear
                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                      ORGANISM: Homo sapien
                                                                                                                                                                                                                              LENGTH: 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 RGMKVLLRVGQ-----SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATS
  5
                                                                             7.1%; Score 130.5; DB Tocal Similarity 22.8%; Pred. No. 0.022; Pred. No. 0.022; Pred. No. 0.022; Pres 67; Conservative 34; Mismatches 1
                                        35 WNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPGVPGPRGEPGAVGPKGPPGVDGVGVPGAAGLPGPQGPSGAKGEPGTRGPPGLIGPTG
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    YDDGNKRWLPAG---TGPQAFSRVQI---
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    -YHNPTANSFRVV----
                                                                                                                        DB 10;
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                                                                                                                     Length 380;
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    -GRKMQ- 55
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CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR APPLICATION NUMBER: BC/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER: OF SEQ ID NOS: 1556

SOCTWARE: PATENTIN Ver. 2.0

SEQ ID NO 979

LENGTH: 674

TYPE: PRT

ORGANISM: Homo sapiens

US-09-925-299-979
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US-09-925-299-979
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                                                                                                                          RESULT 42
US-09-854-133-187
Sequence 187, Application US/09854133
Publication No. US20020183499A1
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 979, Application US/09925299
PATENT NO. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acids, Proteins
                                                                                                                                                                                                            414
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                                                                                                                                                                                                          GGYDFGYDGDFYRADQPRSAPSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLEPGKENLPG-----DPTSNATSRGAEGPLPP-----PSMPAVAGAA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDGTREGLESLQGGVCLTRGMKVLLRVGQSP--RG--GAVPRKPVSEMPME--RDRGAAH 194
                                                                                                                                                                                                                                                                                               SVGPAGPRGPAGPSGPAGKDGRTGHPGTVGPAGIRGPQGHQGPAGPPGPPGPPGPPGVSG
                                                                                                                                                                                                                                                                                                                                       GMGP-----GGAADPPFCPHYEKVSG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGPPGRDGQPGHKGERGYPGNIGPVGAAGAPGPHGPVGPAGKHGNRGETGPSGP--VGPA
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                                                                                                                                                                                                                                                    --- DYGHPVYIVQDGPPQSPPNI 336
                                                                                                                                                                                                                                                                                                                                                                                                                     GGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG-PGSFGRGGSLGL------GGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPAPNILLICORPOLDIRFTIKFQEYSPN-----LWGHEFRSHHDYYIIATSDGTR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.1%; Score 130.5; DB 10; ilarity 27.4%; Pred. No. 0.042; Conservative 20; Mismatches 92;
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US-09-738-973-187
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; ORGANISM: Homo sapien
US-09-854-133-187
                                                                  US-09-738-973-187
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CURRENT APPLICATION NUMBER: U5/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 187
LENGTH: 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 187, Application US/09738973 Patent No. US20020110563A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 69; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                             TYPE: PRT
ORGANISM: Homo
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Lodes, Michael J.
Fling, Steven P.
                                                                                                                                                                                                                                                                                                                                 Algate, Paul A.
Secrist, Heather
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Benson, Darin R.
Elliot, Mark
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                                                                                                                                                                                                                                                                                                                                                                     Raodoh
 7.0%; Score 129; DB 10; Length 595;
27.4%; Pred. No. 0.047;
tive 18; Mismatches 89; Indels 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR PILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 56
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: UNSURE
LOCATION: (758)...(758)
OTHER INFORMATION: Xaa =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1806
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: UNSURE
LOCATION: (809)..(809)
OTHER INFORMATION: Xaa = any amino acid
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722
                                                                                                                                                                                                                        561 QGPRGVQGPPGPTGX-PGKRGRPGADGGRGMPGEPGAKGDRGFDGLPGLPGDKGHRGERG
                                                                                                                                                                                                                                                          169 QSPRGGAVPRKPVSEMPMER-----DRGAAHSLEPGKE-----NLPGD------
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                                                                                                                                                                                                                                                                                              Local Similarity
tes 64; Conserv
 LAGLPGADGPPGHPGKEGQSGEKG-----ALGPPGPQGP 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGRGGGAAGP 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAESPRGWEAGP----
                                   ----GAADPPFCPHYEKVSGDYGHPVYIVQDGP--PQSP 333
                                                                       PGMAGVDGPPGPKGNMGPQGEPGPPGQQGNPGPQGLPGPQGPIGP--
                                                                                                                                                 PQGPPGPPGDDGMRGEDGEIGPRGLPGEAGPRG-----LLGPRGTPGA-----PGQ
                                                                                                                                                                                  ----PTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSE 260
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                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                7.0%;
29.1%;
                                                                                                           --SRHPG-PGSFGRGGSLGL-GGGGGMGPREAEPGELGIALRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 any amino
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                                                                                                                                                                                                                                                                                              Score 129; DB
Pred. No. 0.16;
1; Mismatches
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RESULT 45 US-09-925-302-689 ; Sequence 689, A

Application US/09925302

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens; FEATURE; FEATURE; SITE; NAME/KEY: SITE; LOCATION: (183); OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 46
US-09-978-295A-614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%;
Best Local Similarity 30.9%;
Matches 46; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 614, Application US/09978295A Patent No. US20020156006A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Betstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PA104
                                                                                                                                                                              APPLICANT:
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TYPE: PRT
                                                                                                                                                                                                                                             PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 GVMGP--PGAQGSKGDFGRP----GPP 291
    ဝှု
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KQGATGTPGPQGEKGSKGDGGLIGPKGETG---TKGEKGDLGLPGSKGDRGMKGDA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGAPGPPGPPAEKGAXGAMGRDGATGPSGPQGPPGVKGEAG----
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INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US20020044941A1
                                                                                                                                                                                                                                                                                Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L
                                                                               Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                      Gerber, Hanspeter
Gerritsen, Mary E.
                Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Fong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                                                                 Napier,
                                                                                                                                                                                                                                             Kljavin,
                                                                                                                                                                                                                                                             Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                      Goddard, Audrey
                                                                                                                                                    Paoni, Nicholas F.
                                                                                                                                                                                            win, Ivar J.
Sophia S.
Ler, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                       Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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Pred. No. 0.046;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
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PRIOR APPLICATION NUMBER: 60/07
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/07
PRIOR APPLICATION NUMBER: 60/07
PRIOR FILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/07
PRIOR FILING DATE: 1998-03-20
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CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-03-10
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                                                                                                                                                                                                                   OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/080107
OR APPLICATION NUMBER: 60/080165
OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/080194
OR APPLICATION NUMBER: 60/080327
OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/080327
OR APPLICATION NUMBER: 60/080328
OR APPLICATION NUMBER: 60/080328
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FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/079923
FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
                                                                                      FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
                       FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/
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Sequence 614, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
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Best Local S
Matches 46
  APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 PGAPGPPGPPAEKGAKGAMGRDGATGPSGPQGPPGVKGEAG-----LQGPQGAPG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 RRRAKPSESRHPGP----GSFGRGGSLGLGGGGGMGPREAEPGELGI-----ALRGGG 301
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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/085339
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085323
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/08562
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085700
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085689
OR APPLICATION NUMBER: 60/08569
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085579
OR APPLICATION NUMBER: 60/085570
OR APPLICATION NUMBER: 60/085573
OR APPLICATION NUMBER: 60/085573
OR APPLICATION NUMBER: 60/085570
OR APPLICATION NUMBER: 60/085704
OR APPLICATION NUMBER: 60/085697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
46; Conserv
                                                                                                                                                                                                                                                                                         Fong, Sherman
Gao, Wei-Qiang
Gerber, Hangpeter
Gerritsen, Mary E.
Goddard, Audrey
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                                       Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQGATGTPGPQGEKGSKGDGGLIGPKGETG---TKGEKGDLGLPGSKGDRGMKGDA
                                                                                                           Pan, James;
Paoni, Nicholas F.
                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                               Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
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)R FILING DATE: 1998-04-28

)R APPLICATION NUMBER: 60/083392

)R FILING DATE: 1998-04-29

)R APPLICATION NUMBER: 60/083495

)R FILING DATE: 1998-04-29

)R APPLICATION NUMBER: 60/083496

FILING DATE: 1998-04-2,
APPLICATION NUMBER: 60/083322
TITING DATE: 1998-04-28

APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-27

APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082796 FILING DATE: 1998-04-23

FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082700 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082804

FILING DATE: 1998-04-22

FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15

APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082704 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09

FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203

APPLICATION NUMBER: 60/081817

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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083559
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083500
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
FILING DATE: 1998-04-30

APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06

APPLICATION N FILING DATE: APPLICATION N FILING DATE:

NUMBER: 60/084600 : 1998-05-07

FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/ FILING DATE: 1998-05-07

60/084598

APPLICATION NUMBER: 60/084639 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084640

APPLICATION NUMBER: 60/084441 FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07

: 1998-05-07 NUMBER

PRIOR FILING DATE: 1998-03-31 PRIOR APPLICATION NUMBER: 60/080194 PRIOR APPLICATION NUMBER: 60/080327 PRIOR FILING DATE: 1998-04-01 PRIOR PRILING DATE: 1998-04-01 PRIOR PRILING DATE: 1998-04-01 PRIOR PILING DATE: 1998-04-01 PRIOR APPLICATION NUMBER: 60/08033 PRIOR FILING DATE: 1998-04-01 PRIOR APPLICATION NUMBER: 60/08033 PRIOR APPLICATION NUMBER: 60/08033 PRIOR APPLICATION NUMBER: 60/08033 PRIOR APPLICATION NUMBER: 60/08033 PRIOR APPLICATION NUMBER: 60/08034 PRIOR APPLICATION NUMBER: 60/08034 PRIOR APPLICATION NUMBER: 60/08034 PRIOR APPLICATION NUMBER: 60/08034 PRIOR PILING DATE: 1998-04-08 PRIOR APPLICATION NUMBER: 60/081049 PRIOR PRIOR DATE: 1998-04-08	TILING DATE: 1997-1 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER:	OF INVENTION: Section of INVENTION: Acidate P2630P1C WIT APPLICATION NUMBER FILING DATE: 2001 APPLICATION NUMBER FILING DATE: 1997 APPLICATION NUMBER FILING DATE: 1997 FILING
PRIOR APPLICATION NUMBER: 00/084141 PRIOR APPLICATION NUMBER: 60/084441 PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: 60/084637 PRIOR APPLICATION NUMBER: 60/084637 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084640 PRIOR APPLICATION NUMBER: 60/084598 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084598 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/084627	R PEPLICATION N R PILING DATE: R APPLICATION N R FILING DATE: R APPLICATION N	APPLI A APPLI A APPLI A APPLI A APPLI A FILIN A APPLI A APPLI A APPLI A APPLI A APPLI

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PATENT NO. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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OR APPLICATION NUMBER: 60/084643
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/08533
OR APPLICATION NUMBER: 60/08533
OR APPLICATION NUMBER: 60/08532
OR APPLICATION NUMBER: 60/085323
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085582
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085700
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085689
OR APPLICATION NUMBER: 60/085579
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085579
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46; Conserv
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
                              Stewart,
Tumas, I
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  Williams,
                                                                           Shelton,
                                                                                                                                                                  Pan, James;
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                                               , Margaret Ann
lton, David L.
wart, Timothy A.
                                                                                                                                                                                                                 Sophia S.
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                                                                                                                                Nicholas F.
                                                                                                                                                                                   , Mary A.
     P. Mickey
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Pred. No. 0.061;
9; Mismatches
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR PPLICATION NUMBER: 60/077641
PRIOR PPLICATION NUMBER: 60/077641
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PRIOR PPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077649
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PRIOR PILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/077649
PRIOR PILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/077904
PRIOR APPLICATION NUMBER: 60/07791
PRIOR APPLICATION NUMBER: 60/07893
PRIOR APPLICATION NUMBER: 60/07893
PRIOR APPLICATION NUMBER: 60/07893
PRIOR APPLICATION NUMBER: 60/07966
PRIOR PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/07966
PRIOR APPLICATION NUMBER: 60/07976
PRIOR APPLICATION NUMBER: 60/07972
PRIOR APPLICATION NUMBER: 60/07992
PRIOR PRICING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07992
PRIOR PRICING DATE: 1998-03-3-3
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C9 CURRENT APPLICATION NUMBER: US/09/978,192A CURRENT FILING DATE: 2001-10-15
OR APPLICATION NUMBER: 60/080333
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080334
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/081070
OR APPLICATION NUMBER: 60/081049
OR APPLICATION NUMBER: 60/081049
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OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/080194
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OR APPLICATION NUMBER: 60/080327
OR APPLICATION NUMBER: 60/080328
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FILING DATE: 1998-03-31
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OR FILING DATE: 1998-04-29
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OR APPLICATION NUMBER: 60/083742
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OR APPLICATION NUMBER: 60/084366
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DR APPLICATION NUMBER: 60/083554
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DR FILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/082804
DR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082700
DR FILING DATE: 1998-04-22
DR APPLICATION NUMBER: 60/082797
DR APPLICATION NUMBER: 60/082797
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                                                                                                                             DR FILING DATE: 1998-05-06
RAPPLICATION NUMBER: 60/084441
DR FILING DATE: 1998-05-06
OR APPLICATION NUMBER: 60/084637
DR FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/081071
FILING DATE: 1998-04-08
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083495
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083496
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                                                             APPLICATION NUMBER: 60/084640 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER: 60/083336
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APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/081203
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
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Best Local S
Matches 46
                                         302
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  268
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OR APPLICATION NUMBER: 60/085580
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085573
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085697
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OR APPLICATION NUMBER: 60/085700
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APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
  GVMGP--PGAQGSKGDFGRP----GPP 288
                                       WYDELECEHAEKASCEDACHEAAIAODCEE 330
                                                                                                                             RRRAKPSESRHPGP----GSFGRGGSLGLGGGGGMGFREAEPGELGI------ALRGGG 301
                                                                                     ----KQGATGTPĞPQGEKĞSKĞDĞĞLIĞPKĞETĞ---TKGEKĞDLĞLPGSKGDRGMKĞDA
                                                                                                                                                                         PGAPGPPGPPAEKGAKGAMGRDGATGPSGPQGPPGVKGEAG----
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Similarity 30.9%;
46; Conservative
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Pred. No. 0.061;
9; Mismatches 53;
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Gaps

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214

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RESULT 49
US-09-999-832A-614
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                         APPLICANT:
APPLICANT:
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                                                            Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                     Goddard
                                                                                                                                                              Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                               Filvaroff,
                                                                                                                                                                                                                                                   Botstein, David
Desnoyers, Luc
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Baker Kevin P.
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5. US20020192706A1
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f, Ellen
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APPLICATION NUMBER: 60/084627
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein David
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OR APPLICATION NUMBER: 60/085582
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OR APPLICATION NUMBER: 60/085339

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Roy, Marg
Shelton,
Stewart,
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Godowski, Paul J.
Grimaldi, J. Christopher
                                                           Napier, Mary A.
Pan, James;
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Gerritsen, Mary E.
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Filvaroff, Ellen
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o. US20030004102A1
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Margaret Ann
lton, David L.
vart, Timothy A.
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                                                                                       Sophia S.
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                                            Nicholas F.
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PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077450
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PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/077649
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PRIOR APPLICATION NUMBER: 60/078936
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: PESSOPICT
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1997-10-17
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OR APPLICATION NUMBER: 60/079663
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OR APPLICATION NUMBER: 60/085590
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085580
OR APPLICATION NUMBER: 60/085570
OR APPLICATION NUMBER: 60/085570
OR APPLICATION NUMBER: 60/085697
                                             AADPFCPHYEKVSGDYGHPVYIVQDGPP
GVMGP--PGAQGSKGDFGRP-----
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Gaps

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Search completed: February Job time : 20.5409 secs 11, 2003, 12:13:17

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Result
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  1559
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Query

Match Length DB

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1: sp_archea:*
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Gapop 10.0 , Gapext 0.5
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   671580 seqs, 206047115 residues
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1850
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Q8tbh7 homo sapien
Q90231 brachydanio
Q9pt69 senopus lae
Q9puj4 gallus gall
Q90233 brachydanio
Q90232 brachydanio
Q90232 brachydanio
Q90469 xenopus lae
Q9u474 caenorhabdi
Q9u474 desenorhabdi
Q9u474 drosophila
Q9u474 drosophila
Q9u4786 mus musculu
Q91718 mus musculu
Q91786 mus musculu
Q918411 brachydanio
Q904812 sus scrofa
Q904812 brachydanio
Q90892 mus musculu
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176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 235	61 KFQEYSPNLMGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA 120	116 KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175	1 DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI 60	56 DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI 115	Query Match 84.3%; Score 1559; DB 4; Length 285; Best Local Similarity 100.0%; Pred. No. 3.3e-112; Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0	SEQUENCE 285 AA; 30159 MW; 08D8ACE7142469B2 CRC64;	1 1	C022499; AAH2	Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.	Strausberg R.;	RAIN;	SEQUIENCE FROM N.A.	11		Catarrhini: Hominidae:).		(TrEMBLrel. 21, Last annotation	(TrEMBLrel. 21,	01-JUN-2002 (TrEMBLrel. 21, Created)	Q8TBH7;	Q8TBH7 PRELIMINARY; PRT; 285 AA.	IT 1

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Best Local Similarity
Matches 190; Conserv
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Thomas M.C., Cleary J.A., Brennan C.,
"Morphogenesis of prechordal plate ar
"Morphogenesis of prechordal plate ar
eph/ephrin b signaling.",
Dev. Biol. 234:470-482(2001).
EVBL; AB375227; ABK64277.1; -.
InterPro; IPR001799; Ephrin.
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01-DEC-2001 (
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  Q9PT69;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
PROSTTE; PS01299; EPHRIN; UNKNOWN 1.
SEQUENCE 331 AA; 35638 MW; 6ASEACD509A09818
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ilarity 54.8%;
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RESULT
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Best Local
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Helbling P.M., Saulnier D.M.E., Robinson V., Christian Wilkinson D.G., Brandli A.W.;
"Comparative analysis of embryonic gene expression defineraction sites for Xenopus EphB4 receptors with epi Dev. Dyn. 216:361-373(1999).
EMBL; AJ236866; CAB65511.1; -.
InterPro; IPR002086; Aldehyde dehydr.
InterPro; IPR01799; Ephrin.
Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 192;
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SIGNAL
                                                                                                                                                                       O9PUJ4

O9PUJ4;

O1-MAY-2000 (TrEMBLrel. 13,

O1-MAY-2000 (TrEMBLrel. 13,

O1-JUN-2001 (TrEMBLrel. 17,
                     NCBI_TaxID=9031;
                                                               Archosauria; Aves; Gallus.
                                                                                                       Ephrin-B2 precursor.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ephrin-B3 precursor.

Kenopus laevis (African clawed frog).

Sukaryota, Metazoa, Chordata; Craniata; Vertebrata; Eukaryota, Metazoa, Chordata; Mesobatrachia; Pipoidea; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus.
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01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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PROSITE; PS01299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLV 84
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                                                                                    Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 1
35913 MW;
                                                                                                          Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.7%;
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Last sequence update)
Last annotation updat
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Pred. No. 6.
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4BB0FA39D4C22DCD CRC64;
                                                                                    Craniata; Vert; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                            Vertebrata;
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                                                                                                                                                                            update)
                                                                                       cebrata; Euteleostomi;
Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Christiansen
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ephrin-B ligands.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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Best Local Sim
Matches 135;
Query Match
Best Local Similarity
Matches 141; Conserv
                                               Chan J., Mably J.D., Serluca F.C., Chen J.
Thomas M.C., Cleary J.A., Brennan C., Fis
"Morphogenesis of prechordal plate and no
eph/ephrin b signaling.";
Dev. Biol. 234:470-482(2001).
EMBL; AF375224; AAK4274.1;
InterPro; IPR00179; Ephrin.
Pfam; PF00812; Ephrin; 1.
Prodom; PD002533; Ephrin; 1.
PROSITE; B901299; EPHRIN; UNKNOWN 1.
SEQUENCE 341 AA; 37849 MW; CB522F20E0
                                                                                                                                                                                                                                                                                                            Q90Z33;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
SEQUENCE
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SIGNAL
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"Coding sequence of chicken ephrin-B2.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF180729; AAD53948.1; -.

InterPro; IPR001799; Ephrin.

Pfam; PF00812; Ephrin; 1.

ProDom; PD002533; Ephrin; 1.

PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata
Actinopterygii; Neopterygii;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                          MEDLINE=21290827; PubMed=11397014;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                Ephrin B1
                                                                                                                                                                                                                                                                                                                                                                Q90Z33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMER----- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQYEYYKVYMYDKOQADSCAIRKDNTFLLNCAKFDQDVKFTIKFQEFSPNLWGLEFQKNK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                               CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTNGKSSTTSPFVKDHSGSSTDG--SKAGHSSILGSEVALFÅGIÅSGCIIFIVIIITLVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GALMVLWRTALAKSIVLDPIYWNSSNPKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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333 AA;
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  Conservative
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333 E
; 36761 MW;
          33.3%;
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                                                                                                                                                                                                                                                                                                            19,
  49;
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 Score 616; DB
Pred. No. 1.3e
49; Mismatches
                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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EPHRIN-B2.
; 4C28E8CB211B7783 CRC64;
                                                  CB922F20E0D93E94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 125;
                                                                                                                                                                 Chen J.N., Goldstein N.B.,
J., Fishman M.C., Roberts T
                                                                                                                                                                                                                                                                                                                                                                341
                                                                                                                                                                                                                                                                                                                                                                                                                                                       340
                                                                                                                                                       notochord
             DB 13;
1.3e-39;
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                                                   CRC64;
                         Length 341;
  Indels
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                                                                                                                                                                                                                                                          Cypriniformes;
  38;
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 Gaps
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01-DEC-2001
01-DEC-2001
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ProDom; PD002533; Ephrin; 1.
SEQUENCE 334 AA; 36998 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21290827; PubMed=11397014; Chan J.N., Goldstein N.B., Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B., Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M. "Morphogenesis of prechordal plate and notochord requires intact eph/ephrin b signaling."; eph/ephrin b signaling."; Dev. Biol. 234:470-482(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish)
Bukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
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27 LESIYWNTSNTKFVPGRGVVLYPQIGDKMDIVCPRIK-PGSTEQTNIEYFRVYLVPKEQL
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QIDSMQNGESGGKSG-
                                              --- PPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCW---
                                                                                                                               SLQGGVCLTRGMKVLLRVGQSPRGGAV----PRKPVSEMPMERDRGAAHSLEPGKENLPG
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                                                                                                 NHHGGVCRSKSMKLVLRVGQSPTDSFSAKNHPTRNPPKYPENKDQNTF---
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-ESVGSAGSDVALFAGV--ASGAVIFILIIIALVALLH
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m; Craniata; Veri
; Teleostei; Osta
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Pred. No. 7.9e-39;
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                     Q9U3M2;
Q9U3M2;
Q1-MAY-2000
01-MAY-2000
01-JUN-2002
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Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Ver
Amphibia, Batrachia, Anura, Mesobatrachia,
Xenopodinae, Xenopus.
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MEDILINE=97411149; PubMed=9259557;

MIDILINE=97411149; PubMed=9259557;

Smith A., Robinson V., Pattel K., Wilkinson D.G.;

"The EphA4 and EphB1 receptor tyrosine kinases ar

regulate targeted migration of branchial neural (Curr. Biol. 7:561-570(1997)).
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01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helbling P.M., Saulnier D.M., Robinson V., Wilkinson D.G., Brandli A.W.; "Comparative analysis of embryonic gene expinteraction sites for Xenopus EphB4 recepto Dev. Dyn. 216:361-373(1999).
EMBL; AF128844; AAD32610.1; -. InterPro; IPR001799; Ephrin.
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ProDom; PD002533; Ephrin; 1.
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                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22256 MW;
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                     Created)
Last sequence tast annotated
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ia; Pipoidea; Pipidae;
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Best Local
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Q9U474;
01-MAY-2000
01-MAY-2000
01-DEC-2001
"Genome sequence of the nematode investigating biology. The C. elescience 282:2012-2018(1998).
                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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Chromadorea;
Nematoda; Chromadorea;
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                    epidermal morphogenesis
Cell 99:781-790(1999).
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Pfam; PF00812; Ephrin; 1.
ProDom; PF002533; Ephrin; 1.
SEQUENCE 237 AA; 26748 MW;
                                                                                                                                                                                                        Chisholm A.D.;
"The ephrin VAB-2/EFN-1
                                                                                                                                                                                                                                                   MEDLINE=20084449; PubMed=10619431; Chin-Sang I.D., George S.E., Ding M.,
                                                                                                                                                                                                                                                                                                 STRAIN=N2,
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
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Science 282:2012-2018(1998).
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Lrel. 19,
L protein
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inae; Caenorhabditis.
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Pred. No. 6.1e-
41; Mismatches
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Last annotation update)
Y37E11AR.6).
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                  ode C. el
elegans
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                    elegans: a platform for
ns Sequencing Consortium.
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RESULT 10
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Matches 64
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"Direct Submission.";
"Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF201079; AAR25647.1; -.
EMBL; AC024759; AAK68436.1; -.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
STOIENCE 279 AA; 32068 MW; 8C291A92D97D39EF CRC64;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Bvans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
Bannarides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9V4E1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Dai Y., Kunes S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPHRIN OR CG1862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Miller N., Maggi L.;
"The sequence of C. elegans cosmid Y37EllAR.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ of the EMBL/GenBank/DBJ of the EMBL/GenBank/DDBJ of the EMBL/GenB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "IBolation and Characterization of Drosophila Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DIGPHHHRHHHKKTTTTTTTSTSTS-----TPKTIPPV
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15,
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Last sequence update)
Last annotation update)
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Pred. No. 1.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106
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databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
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RESULT 11
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.F.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylie B.C., Science S.N., Woolage T., Worley K.C., Wu D., Yang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yelf, N. Shong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Shen B. A., Myers B.W., Rubin G.M., Venter J.C.,
RA Shen B.A., Myers B.W., Rubin G.M., Venter J.C.,
RA Shen B.A., Myers B.W., Rubin G.M., Venter J.C.,
RA Shen B.A., Myers B.W., Rubin G.M., Venter J.C.,
RA Shen B.A., Shen B.A., Rubin G.M., Venter J.C.,
RA Shen B.A., Shen B.A., Rubin G.M., Venter J.C.,
RA Shen B.A., Shen B.A., Shen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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ProDom; PD002533; Ephrin; 1.
SEQUENCE 652 AA; 72302 MW;
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InterPro; IPR001799; Ephrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                     PVYIVQD-----GPPQSPPNIY 337
                                                                                                                                                                                    IQPNIIGNHVGTNAVGTGIVGGGGIIL--
                                                                                                                                                                                                                                                                    SMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGPG-SFGRGGSLGLGGGGG
                                                                                                                                                                                                                                                                                                            HVNSHGNNIAIGTNIGINGGQIIGGPQSAGIPINPLSGNNNINGIPTTINSNIDQFNRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                     REGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSL-----EPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNEVVKNESLTYNSGAATSDGNIF
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                                                                                                                                          NG---AYPGHHHIQTGIRINNVPTQHNYPSHKGNANSNINGNDDH----HHYNK---
                                                                                                                                                                                                                                                                                                                                                                                           XDDLYRRIGGRCSTNNMKVVFKVCCAPEDNN-KTTALSNSKSVTDTGGAINVNIANNDES
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Similarity 22.9%;
88; Conservative 5
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Pred. No. 6.1e-06;
D; Mismatches 136
                                                               571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136;
                                                                                                                                                                                                                              -TPGHAHGNINMLQPGRGGI
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Q98TZ1 ID Q AC Q

Q98TZ1;

PRELIMINARY;

PRT;

202 AA

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RESULT 12
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Best Local S
Matches 56
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CT-2001 (TrEMBLrel. 18, Last annotation update)
Ephtin-A6 (Fragment).
Gallus gallus (Chicken).
Gallus gallus (Chordata; Craniata; Vertebrata; Euteleostomi, Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianir
Kawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adult male tongue cDNA, RIKEN full-length enriched library.
clone:2310004J15, full insert sequence.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=TONGUE;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFNA1
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Menzel P., Valencia F., (
"Ephrin-A6, a new ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
PNON_TER
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[1]
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InterPro; IPR001799; Ephrin.
Pfam; proner: entire
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56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232
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visual
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RESULT 13
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RC STEAIN-C57BL/GJ; TISSUE=EMBRYO;

RX MEDINE-C57BL/GJ; TISSUE=EMBRYO;

RX MADINE-C57BL/GJ; TISSUE=EMBRYO;

RX MADINE-C1085660; PubMedd=11217851;

RA ALCAWA J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Coshiwa H.,

RA FleisChmann W., Gaasterland T., King B., Kochiwa H.,

RA FleisChmann W., Gassterland T., Washio I., Pescole G., Quackenbush J.,

RA Kadota K., Matsud Y., Nigisid I., Pescole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Sanida M.F.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Jyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Loc
Matches
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PRINTS; PR01347; EPHRIN.
ProDom; PB002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
PROSITE; PS00678; WD REPEATS 1;
SEQUENCE 205 AA; 23772 MW; 1
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Nature 409:685-690(2001).
EMBL; AK009144; BAB26102.1; -.
MGD; MGI:103236; Effai.
InterPro; IPR001799; Ephrin.
InterPro; IPR001680; WD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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Rodentia;
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Pred. No. 2.3e-
34; Mismatches
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Sciurognathi; Muridae;
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76;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                             K. -F.,
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                                                                                          Query Match
Best Local S
Matches 106
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Best Local S
Matches 61
                                                                                                                                                                                                                             Mamm. Genome 11:1087-1092(2000).
EMBL; AF222861; AAF37271.1; -.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF00386; C1q; 1.
Pfam; PF00391; Collagen; 8.
PRINTS; PR00007; COMPLEMNTC1Q.
ProDom; PD000007; COLLagen; 2.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9N178;
01-OCT-2000
01-OCT-2000
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
PRODOm; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
SEQUENCE 206 AA; 22859 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
EMBL; aK012195; BAB28092.1; -.
MGD; MGI:106643; Efna4.
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9N178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21015405; PubMed=11130976;
Nielsen V.H., Bendixen C., Arnbjerg
Shukri N.M., Thomsen B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki
"Functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Abnormal growth plate function in pigs carrying a dominant mutation in type X collagen.";
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  212
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                                                                                                                 Local Similarity
                                             <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEAPPAPNL-LLTCDRPDL---DLRFTIKFQEVSPNLWGHEFRSHHDYYIIATSDGTREG 147
     MGPP--GPPGV-
                                          MGPPHSGPGGYRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQI-GDR-L 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAEGANSFORWNCSMPFAPFSPVRFSEKIORYTPFPLGFEFLPGETYYYISVPTPESPG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIYWNSSNPRL-LRGDAVVELGFNDYLDIFCPHYESPGPPEGP--ETFALYIVDWSGYEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 8.8%; Sc
Similarity 28.1%; Pr
61; Conservative 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O (TrEMBLrel.
O (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                          675
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                                                                                     8.4%; Score 156; DB 6; larity 28.6%; Pred. No. 0.00063; Conservative 17; Mismatches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                       AA;
                                                                                                                                                                                          65447 MW;
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Last sequence update)
Last annotation update)
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Pred. No. 4.3e.
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                          26397B10310383F9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------KESGSSHESAHP-----VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194
-GKR--GENGFPGQPGIKGDRGF 240
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                                                                                          118;
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                                                                                                                                       Length
                                                                                                                                                                                          CRC64
                                                                                             Indels
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Sus.
                                                                                                                                          675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jensen
                                                                                          130;
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                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    093431;
01-NOV-1998
01-NOV-1998
01-DEC-2001
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Brachydanio rerio (Zebrafish) (Zebra danio).

Bukaryota, Metazoa; Chordata, Craniata; Verrebrata, Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform,

Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01347; EPHRIN.

Prodom; PD002533; Ephrin; 1.

PROSITE; PS01299; EPHRIN; 1.

PROSITE; PS00290; IG MHC; UNKNOWN 1.

SEQUENCE 229 AA; \( \frac{7}{2}6115 \) MW; \( 86\frac{8}{6}4462F67AF6F5C \) CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001799; Ephrin.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00812; Ephrin; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ006838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the somites."
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"Eph signalling is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7955;
                                                       134
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                                                                                                                                                              83
                                                                                                                                                                                                             93
                                                                                                                                                                                                                                                                                                         33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC
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                                                       PLHHHGQECLRLKVDVV-----GPHGSKNKKKMVEKVEEIEGKMAAGGVHNPSNRLPADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPGPVGPAGAKGVPGHNGEÅGPRGAPGIPGTRGPIGPPGIPGFPGSKGDPGNP-----
                                                                                                                                                                                                        EAPPAPNLLLTCDR----PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPQSPPNIYYK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M----GPREAE--PGELGIA-LRGG------GAADPPFCPHYEKVSGDYGHPVYIVQDG
                                                                                                      SL--QGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDP
                                                                                                                                                              KPHSFDQLRWECSRPFAPHAPEKFSEKFQRFTPFTLGKEFRQGESYYYIS-----K
                                                                                                                                                                                                                                                                  VYWNSTNANFLWD-DYTVDVRINDYLDIICPH-YAHGEIASQEAERYVLYMVELEDYENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PP-GPAGIATK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGLALLLLGVAGAGGAMCWRRRR---AKPSESRHPG-----PGSFGRGGSLGLGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                8.4%;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                Score 155; DB 13;
Pred. No. 0.00022;
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K., Cooke J.;
segmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 229;
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208

TSNATSRGAEGPLPPPSMPAVAGAAG

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ACCONCRETE TO THE PROPERTY OF 
        RESULT 17
Q9IB91
ID Q9IB9
AC Q9IB9
DT 01-0C
DT 01-0C
DT 01-JU
DE Type
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Best Local S
Matches 86
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MEDIINE-20536494; PubMed=10965041;

Saito K., Naito I., Seki T., Ochashi T., Kimu Kishiro Y., Sado Y., Yoshioka H., Ninomiya Y.

"Differential Expression of Mouse a5(IV) and Epithelial Basement Membranes.";

J. Biochem. 128:427-434(2000).

EMBI; AB041350; BAB13673.1; -.
Q9IB91;
01-0CT-2000 (TrEMBLrel. 15, C
01-0CT-2000 (TrEMBLrel. 15, L
01-JUN-2002 (TrEMBLrel. 21, I
Tyme I collagen alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ESQ2

Q9ESQ2;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
7 70 collagen alpha 5 chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM
Collagen.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01413; C4; 2.
Pfam; PF01391; Collagen; 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:88456; Col4a5.
InterPro; IPR000087; Collagen.
InterPro; IPR001442; ProcollagnC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POIGDREDIECPRARPPGPHSSPNYEFYKLYLVGGAOGRRCEAPPAPNHLETCDRPDLDE 111
                                                                                                                                                                                                                                                                                                                           ELGI----ALRGGGAADPPFCPHYEKVSGD----YGHPVYIVQDGPPQSP
                                                                                                                                                                                                                                                                                                                                                                             KGIQGVAGNPGQPGLPGPKGDPGQTITQPGKPGLPGSPGRDGEVGLPGDPGLPGQPGLPG
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; PD003923; ProcollagnC4; 1.
SM00111; C4; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    -LLGVAGAGGAMCWRRRRAKPSES-RHPG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1691 AA;
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                         Created)
Last sequence update)
Last annotation updat
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Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PGSFGRGGSLGLGGGGGMGPREAEPG
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Lya Y.;
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                                           update)
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Best Local S
Matches 86
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Pfam; PF00193; Vac; 1.
Pfam; PF00093; Vac; 1.
ProDom; PD000007; Collagen; 2.
ProDom; PD000078; Fib collagen_C; 1
SWART; SM00038; COLFI; 1.
SWART; SM00214; VWC; 1.
                                                                                                                                                                                     O17036
O17036;
O17036;
O17036;
O17036;
O17JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JAN-2002 (TrEMBLrel. 21, Last annotation updat
""mothetical 31.6 kDa protein.
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Collagen.
SEQUENCE 1447 AA.
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"Expression and characterization of Kenopus type I colla
(COLLAI) during embryonic development.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AB034701; BAA94972.1; -.

InterPro; IPR0000887; Collagen.

InterPro; IPR000885; Fib_collagen_C.

InterPro; IPR001087; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1021
             SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
                                                                                                                                              Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
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[1]
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                                                                                                                NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGEAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPGPHSSPNYEFYKLYLVG-------GAQGRRCE-APPAPNLLLTCDRPDLDL
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                     PubMed=9851916;
                                                                                                                                              Nematoda; Chromadorea; Rhabditida; rinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A4A6DD2B4158E38B CRC64;
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Gaps

16;

1020

970

261 911 202

851

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RESULT 19
Q17208
ID Q17208
AC Q17208;
DT 01-NOV-
DT 01-UN-
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Best Local &
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ da
EMBL; AF022985; AAB69961.1; -.
InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col_cuticle_N.
Pfam; PF01391; Collagen; 3.
Pfam; PF01391; Collagen; 1.
Hypothetical protein.
SEQUENCE 325 AA; 31591 MW; 6538D4E37C9EC202
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=EUROPEAN 200X300; TISSUE=IMAGINAL WING DISC;
STRAIN==97148965; PubMed=8995790;
MEDLINE=97148965; PubMed=8995790;
Chareyre P.P., Besson M.M., Fourche J.J., Bosquet G.G.;
Chareyre P.P., Besson M.M., Fourche J.J., Bosquet G.G.;
"Identification of a Bombyx collagenous protein with multiple
                                                                                                                                                  Bombyx mori (Silk moth).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Bombycoidea; Bombycidae; Bombyx.

NCBI TaxID=7091;
                                                                                                                                                                                                                                                        017208;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2002 (TrEMBLrel. 21,
Collagen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pauley A., Gattung S.;
"The sequence of C. elegans
Submitted (SEP-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGP-AGGPGQPG---HSGGAGSPGPQGP----PGPSGQPGHSGNDGVPGAPGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GPREAEPGELGIALRGGGAADP-PFCPHYEKVSGDYGHPVYIVQDGPPQSPPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGGLALLILIGVAGAGGAMCWRRRRAKPSESRHPG-PGSFGRGG--SLGLGGGGGM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPAGAPGPAGP-----PGA----PGPKGNNGQPGAPAQS-GGRGP-PGPRGP--A 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSASTLVTVASAASGIAIVVCVFTVGMIFNDINSFYDEKIGELKEFKGYEQIA--WQAMI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PGOPGAPGEOGHPG-----LAGOPGSGARINPATGRPGFCIT------ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQG--GVCLTRGMKVLLRVGQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTTRPSSGSS-----FLIGRNKRQAQCNCGAQSRGCPAGPPGP------96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRARPPGPHSSPNYEFYKLYLVG------GAQGRRCEA-PPAPNLLLTCDRPDLDL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92;
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Last annotation updat
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     Created)
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Pred. No. 0.00095;
                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                             569
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Best Local Similarity
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Insect Biochem. Mol. Biol. 26:67
EMBL; Z30348; CAA83002.1; -.
InterPro; IPR001087; Collagen.
InterPro; IPR001419; Glutenin.
Pfam; PF01391; Collagen; 5.
PRINTS; PR00210; GLUTENIN.
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Q19111;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                           MMBL; COLLEGE. IPRO00087; Collagen. InterPro; IPRO02486; Col_cuticle_N. InterPro; IPRO02486; Col_cuticle_N. Pfam; PP01391; Collagen; 2. Ffam; PP01484; Col_cuticle_N; 1. SECUTENCE 316 AA; 29444 MW; 4D7/
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 282:2012-2018(1998).
EMBL; Z67990; CAA91932:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F02D10.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Genome sequence of the nematode
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                                        276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nvestigating biology.
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                                        GLGGGGGMGPR------EAEPGELGIALRGGGAADPPFCPHYEKVSG
                                                                                    PGPAGPPGNDGQPGQPGGPG--QDGASSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPREAEPGELGIALRG----GGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
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                                                                                                                                    EGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP-GSFGRGGSL
                                                                                                                                                                               GASGKGAÄAPCEPSTPPPCQ-PCPÄGPPGPPGPDGTPGEPGGPGPAGSPAGPSGPGPAGP
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                                                                                                                                                                                                                                                                          49;
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(NOV-1995)
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Pred. No. 0.00
14; Mismatches
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Pred. No. 0.00
| Pred. No. 0.00
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Q61434;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
                   Q91718;
Q91718;
01-NOV-1996
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01-JUN-2002
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SEQUENCE
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"Identification of a novel collagen chain represented by extensive interruptions in the triple-helical region.";
Cell. Mol. Biol. Res. 196:576-582(1993).
EMBL; D17546; BAA04483.1; -.
HSSP; P39061; INCE
MGD; MGI:88449; Coll531.
InterPro; IPR000087; Collagen.
Ffam; PF01391; Collagen; 8.
Pfam; PF01391; Collagen; 8.
Pfam; PF02210; TSPN. 1.
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Mammalia; Eutheria; Rodentia;
MCBI TaxID=10090;
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    Alpha-1
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                                                                                                                                                                                                                                 DDMEGS-GIPLWTTARSSDGLQGPPGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGKENLPGDPTSNATSRGAEGP--LP-PPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSGFSGDIESLRG-----
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type
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6 (TrEMBLrel.
2 (TrEMBLrel.
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5 (TrEMBLrel. 01, 05 (TrEMBLrel. 01, 12 (TrEMBLrel. 21, 12 (TrEMBLrel. 21, 15 ) oe II' collagen.
                                                                                                                 PRELIMINARY;
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                          sequence update) annotation updat
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Pfam; PF0139; Collagen; 18.

Pfam; PF00093; vvc; 1.

ProDom; PD000007; Collagen; 3.

ProDom; PD002078; Fib collagen_C; 1

SWART; SW00038; COLFI; 1.

SWART; SM00214; VWC; 1.
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Collagen.
SEQUENCE
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J. Cell Biol. 118:565-575(1991).
EMBL; M63596; AAA49679.1; -.
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MEDLINE=92011898;
Su M.W., Suzuki H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphila; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI TaxID=8355;
[1]
                                                                                                               alpha 1(XVIII)
chain.";
                                                                                                                                TISSUE=PRIMARY TAIL CULTURE;

MEDLINE=94245707; PubMede8188673;

Rehn M., Hintikka E., Pihlajaniemi T.;

Rehn M., Hintikka E., Pihlajaniemi T.;

"Primary structure of the alpha 1 chain of mouse type XVIII collagen,

partial structure of the corresponding gene, and comparison of the
alpha 1(XVIII) chain with its homologue, the alpha 1(XV) collagen
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                        SEQUENCE OF 1-562 FROM N. MEDLINE=94240112; PubMed=
                                                                                             J. Biol.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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    Pihlajaniemi
                                                                                             Chem.
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nilarity 31.1%;
Conservative .1:
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                                                                                             269:13929-13935(1994).
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                           PubMed=8183894;
                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142495
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Pred. No. 0.000
L1; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; | Sciurognathi; Muridae;
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VIII collagen)
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         during Xenopus production of
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Best Local S
Matches 92
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J. Biol. Chem. 270:4705-4711(1995)

EMBL; U03715; AACS2903.1; JOINED.

EMBL; U03716; AACS2903.1; JOINED.

EMBL; U04607; AACS2903.1; JOINED.

EMBL; U34608; AACS2903.1; JOINED.

EMBL; U34609; AACS2903.1; JOINED.

EMBL; U34610; AACS2903.1; JOINED.

EMBL; U34610; AACS2903.1; JOINED.

EMBL; U34611; AACS2903.1; JOINED.

EMBL; U34612; AACS2903.1; JOINED.

EMBL; U34613; AACS2903.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01391; Collagen; 8.
Pfam; PF01392; Fz; 1.
Pfam; PF02210; TSPN; 1.
ProDom; PD000007; Collagen; 1
SWART; SW00282; LamG; 1.
SWART; SW00282; LamG; 1.
SWART; SW00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagenous with type XV Proc. Natl. [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDLING TO THE MEDITION TO THE MEDITION TO THE MEDITION OF THE MEDITION OF THE MEDITION TO THE
                   1048
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PROSITE; PS50038; FZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000087; Collagen.
InterPro; IPR000024; Fz_domain.
InterPro; IPR001791; Laminin_G.
InterPro; IPR003129; TSPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-562 FROM N.A.
MEDLINE=95181468; PubMed=78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Alpha 1(XVIII),
                                                                                                                                                                                                                                                                                                                  872
                                                       312
                                                                                                                                                                    952
                                                                                                                                                                                                     198
                                                                                                                                                                                                                                           909
                                                                                                                                                                                                                                                                             141
                                                                                                                                                                                                                                                                                                                                                                                            822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:88451;
                                                                                                                                                                                                                                                                                                                                                                                        --PGAQGPPGPQGPPGKD-----GTPGRDGEPGDPGEDGRPGDTGPQGFPGTPGDVG
                                                                                                                                                                                                                                                                                                                                                                                                                             LCPRAR-PPGPHSSPNYEFYKLYLVGGAQGRRCE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPP--GPAGPQ-----GPAGPVVQSPNSQPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPHSGPGGVRVGALLLLGVLG-LVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                 DDMEGS-GIPLWTTARSSDGLQGPPGSP
                                                     EKVSGDYGHPVYIVQ-----DGPPQSP
                                                                                                                            RAKPSESRHPGP-GSFGRGGSLGLGGGGGGGGGREAEPGELGIALRGG--GAADPPFCPHY
                                                                                                                                                                    PGPAGLPGVP-----GKEGPPGFPGPPGPPGPPGREGP----PGVAGQKGSV----
                                                                                                                                                                                                     PGKENLPGDPTSNATSRGAEGP--LP-PPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRR
                                                                                                                                                                                                                                                                             SDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP--VSEMPMERDR-GAAHSLE
                                                                                                                                                                                                                                                                                                                  PKGEKGDPGIGPRGPPGP
                                                                                                                                                                                                                                                                                                                                                      ----APPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
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                                                                                           GDVGIPGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1774 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen chain with frequent interruptions in the re, a distinct tissue distribution, and homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182229 MW;
                                                                                         GDLGPIGMPGKSGLA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 146.5;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF4D9BC9E88EF232 CRC64;
                                                       333
                                                                                                                                                                                                                                           PRGFPGPPGPPGLPGEPGRFGINGSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ends of type XVIII collagen chains the expression of the corresponding ins a novel motif homologous to rat
                                                                                           GSPGPVGPPGPPGPPGPGFAAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107;
                                                                                                                                                                                                                                                                                                                  PGPPGPSFRQDKLTFIDME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1774;
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Best Local &
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01-MAY-2000
01-MAY-2000
01-JUN-2002
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SEQUENCE
                                                                                                                                                                                                                         Alpha 3
COL4A3.
                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                           collagen
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TISSUE-KINEY,

MEDLINE-20005934; PubMed=10534397;

MEDLINE-20005934; PubMed=10534397;

Lu W., Phillips C.L., Killen P.D., Hlaing T., Harrison Lu W., Phillips C.L., Kollen P.D., Hlaing T., Harrison Lu W., Phillips C.L., Coverbeek P.A., Meisler M.H.;

"Insertional mutation of the collagen genes col4a3 and model of alport syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q90800 PRELIMINARY; PRT; 675 AA.
Q90800,
Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Collagen-alpha-3 type IX precursor.
Collagen-alpha-3 type IX precursor.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X64712; CAA45967.1; -. InterPro; IPR000087; Collagen. Pfam; PF01391; Collagen; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=CARTILAGE;

MEDLLNE=92241276; PubMed=1572350;

Brewton R.G., Ouspenskaia M.V., van der Rest M., Mayne R.;

"Cloning of the chicken alpha 3(IX) collagen chain complet primary structure of type IX collagen.";

Eur. J. Biochem. 205:443-449(1992).
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000007; Collagen; 3.
Collagen; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAVAGAAG--GLALILLGVAGAGGAMCWRRRRAKPSESRHPG------PGSFGRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVG--PQGPPGPRGPPGPSGKDGIDG----EPGPSGLPGPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGPPGPPGMPGPKGHTGHKGEPGETGKEGEKGSPGPPGPPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GAADPPFCPHYEKVSGDYGHPVYIVQDGP-----PQSPPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GSLGLGGGGGM----GPR-----EAEPGELGIALRGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGPPGPPGPSGLPGGNGFRGPPGPSGLPGFPGPPGPPGLAGIIPEGGGDLQCPALCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGAAGEAGLPGLP----GVDGLTGT-----DGPPGPNGPPGDRGALGPAGPPGPAGKGL
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22
675 AA;
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675 C
63069 MW;
                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.9%;
                                                                                                                                                                                                                                                                                                                            13,
13,
21,
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                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 146;
Pred. No. 0.
                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                             col4a4
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RESULT 26
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Best Local
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 61:113-124(1999).
EMBL, AF169387; AAD590449.1; -.
EMBD; MGI:104688; Col4a3.
InterPro; IPR000087; Collagen.
InterPro; IPR001442; ProcollagnC4.
InterPro; IPR000504; RNA_rec_mot.
"Genome sequence of the nematode investigating biology."; Science 282:2012-2018(1998).
EMBL; Z81503; CABO4111.1; -.
                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
F14F7.1 protein.
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                                                            SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                McMurray A.A.;
Submitted (NOV-1996)
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           017805
                                                   none;
                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                  F14F7.
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                                                                                                                                                                                                                                                                                                                                                            GAADPPFCPHYEKVSGDYGHPVY---IVQDGP--PQSPP 334
                                                                                                                                                                                                                                                                                                                                                                                                             RRAKPSESRHPG-PGSFGRG-----
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97; Conserv
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                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                             PubMed=9851916;
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                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation updat
                                                                                                 EMBL/GenBank/DDBJ
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Pred. No. 0
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                                    platform
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RESULT 27
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Query Match
Best Local Similarity
Matches 46; Conserv
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Q94620;
                                                                                                                               Collagen.
                                                                                                                                                                                                                                                                                                     Wang T., Deom C.M., Hussey R.S.; "Identification of a Meloidogyne incognita cuticle collagen gene are "Identification of the developmental expression of three collagen genes in parasitic stages."; Mol. Biochem. Parasitol. 93:131-134(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meloidogyne incognita (southern root-knot nematode).
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne
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01-FEB-1997 (TrEMBLrel. 02,
01-DEC-2001 (TrEMBLrel. 19,
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InterPro; IPR002486; Col cuticle N.
Pfam; PF01484; Col cuticle N; 1.
SEQUENCE 305 AA; 29497 NW; 161BFA90D024C2E6 CRC64;
                                                                                                    SEQUENCE
                                                                                                                                                                           Pfam; PF01391; Collagen; 2.
Pfam; PF01484; Col_cuticle_N; 1.
                                                                                                                                                                                                         EMBL; U68729; AAC48358.1; -
InterPro; IPRO000087; Collagen.
InterPro; IPR002486; Collauticle_N.
Pfam; PF01391; Collagen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98324411; PubMed=9662034; Wang T., Deom C.M., Hussey R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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  7.9%; Score 145.5; DB 5; 28.4%; Pred. No. 0.0017; rative 14; Mismatches 67;
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29361 MW;
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                                                                                                                                  COLLAGEN
                                                                                                    825AEF0249FDFC78 CRC64;
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Matches 87
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml I.M., Staubli F., Suzuki R., Tonita M., Wagner I., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carminci P., de Bonaldo M.F.,
A Blake J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,
A Blake J., Balt C., Fletcher C., Fujita M., Gariboldi M.,
A Blake J., Balt D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustinnich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibate Y., Storch K.-F.,
A Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Havashtzaki Y., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collagen.
SEQUENCE
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STRAIN=C57BL/6J; TISSUE=EMBRYO;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K.,
Kawai J., Shinagawa A., Shibata K.,
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                                                                                                                                                                                                                                                                                 GPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVXWNSANKRFQAEGGYVLYPQIGDRLDLL 61
                                       FQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQG--GVCLTRGMKVLLRVGQSPRGG
                                                                                                    CPNSCPPGRSGYPG-----LPGMRGHKGAKGEIGE-----
                                                                                                                                                               CPRARPPGPHSSPNYEFYKLYLVG-----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIK 116
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2 (TrEMBLrel.
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J. Biol. Chem. 275:8749-8759(2000).
EMBL; AF177941; AAF59902.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                   24;
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InterPro; IPRO0087; Collagen_C.
InterPro; IPRO0085; Fib collagen_C.
InterPro; IPRO0185; Fib collagen_C.
InterPro; IPRO01791; LamInin_G.
InterPro; IPRO03129; TSPN.
Pfam; PF01410; COLPI; 1.
Pfam; PF01410; COLPI; 1.
Pfam; PF02210; TSPN; 1.
ProDom; PF002210; TSPN; 1.
ProDom; PF0022078; Fib_collagen; 3.
ProDom; PF0020078; Fib_collagen_C; 1.
SMART; SM002038; COLPI; 1.
SMART; SM002038; COLPI; 1.
SMART; SM00210; TSPN; 1.
SMART; SM00210; TSPN; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-PLACENTA, AND HEART;

MEDLINE=20187594; PubMede10722718;

Imamura Y., Scott I.C., Greenspan D.S.;

"The pro-alpha3 (V) collagen chain. Compexpression domains in adult and develop the structures and expression domains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 MPAVAGAAG-----GLALL--LLGVAGAGGAMCWRRRRAKPSE-----SRHPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 GIPGAAGDQGQRGPPGETGPEGDRGI-----QGSRGIPGSPGPKGDTGLPGVDGRDGIPG
                                            TIKFOEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRG
                                                                                                                                            LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCE-----APPAPNLLLTCDRPDLDLRF 113
                                                                                                                                                                                                ĠPPGHQGKDG-RPGHPGQRGELG------FQGQTG-----FQGQTG------
                                                                                                                                                                                                                                                  GPP-HSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - PGSFGRGGSLGL-GGGGGMGPREAE--PGELGIALRGG--GAADPPFCPHYEKVSGDYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PGRQGHKGEEGDQGELGEVGDQGPPGPQGLRGITGIVGDKGEKGARGFDGEPGPQ
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                                                                                                                                                                                                                                                                                                                            7.8%; Score 145; 24.0%; Pred. No. 0.

    Created)
    Last sequence update)
    Last annotation update)
    chain.

                                                                                             VLGPQGKTGEVGPLGERGPPGP
                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            SE8FF97135397AC1 CRC64;
--- EQGLPGLEG----
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                                                                                                                                                                                                                                                                                                   103; Indels
                                                                                                                                                                                                                                                                                                                                                     Length 1745;
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--REGAKG
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959
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RESULT
Q96QB3
ID Q99
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AC 01
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Best Loc
Matches
                                                                                                                Q96QB3 PRELIMINARY;
Q96QB3;
Q1-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-JUN-2002 (TrEMBLrel. 21, L
Type V preprocollagen alpha 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996
01-NOV-1996
01-DEC-2001
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                                                                                                 Type V
COL5A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOl. Biochem. Parasitol. 83:121-124(1996).
EMBL; U40766; AAC47437.1; -.
InterPro; IPR000087; Collagen.
InterPro; IPR0002486; Col_cuticle_N.
Pfam; PF01391; Collagen; 2.
Pfam; PF01391; Collagen; 1.
SEQUENCE 309 AA; 29472 Mw; 0C6C9D5BA76C8916 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q25466;
Q25466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1123
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                           Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97164124; PubMed=9010847; Ray C., Wang T.Y., Hussey R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meloidogyne incognita (southern root-knot nematode).
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
NCBI_TaxID=6306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        206
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                                                                                                                                                                                                                                                                                                                                                       QPGG-----PGQPGSPA-QSQEAGPAPPGPPGDAGAPGQPGNPGPAGQPGGPGGPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGLALLLIGVAGAGGAMCWRRRRAKPSESRHPG----PGSFGRGGSLGL-GGGGGMGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCPGGQPGQPGPPGPPGQPGGPGQPGGQASPGEP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e collagen gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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5 (TrEMBLrel. 01,
1 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      EAEPGELGIALRGGGAADPPFCPHYEKVSG
                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                   Last sequence update)
Last annotation update)
2 chain (Fragment).
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Last sequence up
Last annotation
                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 144.5;
Pred. No. 0.00
L4; Mismatches
                              Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                             1347
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                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meloidogyne
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                              Euteleostomi;
; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GPAGPPGSPGAPG
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                           RESULT 32
Q90W37
ID W90W3
AC Q90W3
AC Q90W3
AC Q90W3
DT 01-DE
DT 01-JU
DE Alpha
GN COL2A
OS Gallu
OC Enkar
OC Archo
OC Gallu
OC Archo
CO Gallu
COX NCBI
RD SEQUE
RA S
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SEQUENCE TISSUE=STERNAL;

TISSUE=STERNAL;

Caixia X., Yongzhi X., Siqi G., Yiying x
Submitted (JUL-2001) to the EMBL/GenBanl
REMBL, AV046949, AAK98621.1;
R InterPro; IPR000087; Collagen.
R InterPro; IPR000885; Fib collagen.
C.
R Ffam; PF01491, COLPE; 1.

DR Pfam; PF01391; Collagen; 18.
DR ProDom; PD000007; Collagen; 6.
DR ProDom; PD002078; Fib_collagen_C; 1.
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Best Local :
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EMBL; AY016295; AAL13166.1; JOINED.
EMBL; AY016299; AAL13166.1; JOINED.
EMBL; AY016299; AAL13166.1; JOINED.
EMBL; AY016291; AAL13166.1; JOINED.
EMBL; AY016292; AAL13166.1; JOINED.
EMBL; AY016292; AAL13166.1; JOINED.
EMBL; AY016293; AAL13166.1; JOINED.
EMBL; AY016293; AAL13166.1; JOINED.
EMBL; AY016293; AAL13166.1; JOINED.
InterPro; IPR000087; Collagen.
InterPro; IPR0000885; Fib_collagen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                             Q90W37; PRELIMINARY;
Q90W37; Q10D2
01-DEC-2001 (TrEMBLrel. 19, L
01-DEC-2001 (TrEMBLrel. 19, L
01-UN-2002 (TrEMBLrel. 21, L
Alpha 1 type IIA collagen pre
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Archosauria; Aves; l
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Collagen.
NON_TER 1
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Pfam; PF01391; Collagen; 18.
ProDom; PD000007; Collagen;
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
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MEDLINE=21451029; PubMed=11566270;
Melkoniemi M., Kvist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG-PGSFG-RG--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGPRGDPGTVGPPGPVGERGAPGNRGF----PGSDGLPGPKGAQGERGPVGSSGPKGSQ
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1347
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                                                                                                                                                                                                                                                                                                                                                       ; Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor
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                                                                                                                                                                                           G., Yiying S.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 144.5; I
Pred. No. 0.01:
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F25F20E6BB23A17C CRC64;
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                                                                                                                                                                                              databases
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collagen genes.";
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Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collagen;
SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9F342;
Q9F342;
                                                                                                                                                                                                                                                                                                                                                           Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch S., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.

Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UIN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SCO5128.
SCO5128 OR SC9E12.13.
                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL391751; CAC05758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
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                            LTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGM 161
                                                                                                                                                       PPHSGPG-----GVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAMCWRRRRAKPSESRHPG-PGSFGRGGSLGLGGGGGGGGGPREAEPGELGIALRGG----
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                                                                                           YPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQ-----GRRCEA---PPAPNLL 101
                                                                                                                           PRKSGPGKGTQGGGSTNGAGLPAGSAPTAGTPGAAGARGAGPAGASGAG------
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                                                            ARPGGGSGRPGGVVGSMNAPGGARSGSAGGGARSGATGGPVAP--- 224
                                                                                                                                                      7.8%; SCULT 23.5%; Pred. No. 0.vvc. 130; ative 23; Mismatches 130;
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28.1%;
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134999
                                                                                                                                                                                                                                                      75820 MW;
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MW; 88D9AAB17F214FF5
                                                                                                                                                                                                     Score 143.5; DB 16;
Pred. No. 0.0068;
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-GGGTGSFDVTEALAAGPLGGNGN 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00111; C4; 2.
Collagen.
SEQUENCE 1747 AA; 1
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01-NOV-1996 (TrEMBLrel. 0
01-JUN-2002 (TrEMBLrel. 2
Alpha2(IV)-like collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            urchin .alpha.2(IV)-like collagen cha

J. Biol. Chem. 269:33167-13171(1994).

EMBL; X76730; CAA54146.1; -.

InterPro; IPR000087; Collagen.

InterPro; IPR001442; ProcollagnC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF01413; C4; 2.
Pfam, PF01391; Collagen; 21.
ProDom, PD000007; Collagen, 6.
ProDom; PD003923; ProcollagnC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus purpuratus (Purple sea urchin)
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q26640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a cell lineage-specific urchin .alpha.2(IV)-like collagen chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exposito J.Y., Suzuki H., Geourjon C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94230414; PubMed=8175744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strongylocentrotus.
     466
                                                                                                                                                                                                                                                                                                                                  322
                                                                                                                                                                                                                                                                                                                                                                                                                                          266
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                                                      233 GGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG------PGSFGRGGSLGLGGGGGMGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 PDNISGNTVTSGIPVVPGERTAPFPAGSGDGPRPHTPPKL 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
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                                                                                                                                                                                                                                                                                                                                                                              PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GPRGMDG----MKGATGEVGDLGSYGDYGEKGLPGYSGERGFPGNPGIPGLLGMNGEKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRAR
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G-----FMGQKGGRGP----PGRAGPAGPARSGNQSFQGFPGDTGNTGLKGMRGIQGALG
                                                                                                                                                              EMPMERDRGAAHSLEPGKENLPGDP----TSNATSRGAEGPL----PPPSMPAVAGAA
                                                                                                                                                                                                                                                                            HEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ----SPRGGAVPRKPVS
                                                                                                                                                                                                                                                                                                                             -DGPQGRPGYDGYK--GPSGDYGMDGDPGPAPDI------------
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                                                                                                             SQGEGRÓGEKGESGRPGI PGFQGETGERGNDGNFGERGEKGNMGESRPGPPGMDGSRGRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1747 AA; 173312 MW;
                                                                                                                                                                                                                  -EEIVVGVGPPGDEGPPGNPGPRGFSGAIGLFGDQGQPGYPGPMGGPGPRGPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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24.1%; Pred. No. 0.011,
74+1ve 24; Mismatches 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EE722E878394B9B6 CRC64;
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Best Local Sim
Matches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Strausberg R.;

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, BC013581; AAH13581.1; -.

R InterPro; IPR001073; C1q.

R InterPro; IPR001087; Collagen.

R Pfam; PF00386; C1q; 1.

R Pfam; PF01391; Collagen; 7.

R ProDom; PD00007; Collagen; 2.

R ProDom; PD00007; Collagen; 2.

R ProDom; PD001113; C1Q; UNKNOWN 1.

Collagen; Hypothetical protein.

O SEQUENCE 744 AA; 73364 MW; 2BC1B0955DE2C9A3 CRC64;
01-CCT-2000 (TrEMBLrel. 15, Creat 01-CCT-2000 (TrEMBLrel. 15, Last 01-UN-2002 (TrEMBLrel. 21, Last 01-UN-2002 (TrEMBLrel. 21, Last Alpha 1 (V) collagen. Gallus gallus (Chicken). Eukaryora; Metazoa; Creat Marchosauria; Aves; Neognathae; Garchosauria; Aves; Neognathae; G
                                                                                                                                                                                     Q9IAU4;
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Q96D07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PGMHG-PPGPVGLPGVGKPGVTGFPGPQGPLGKPGAPGEPGPQGPIGVPGVQGPPG
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Pred. No. 0.000
16; Mismatches
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     Q25582
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AC Q2558
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DT 01-NO
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DT C11-JU
DE CCLOS
GN CCLOS
GN TClad
OC Entar
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Přám; PPÖ139; COLIAGEN; 19.

Přám; PPÖ2210; TSEN; 1

ProDom; PD000007; COLIAGEN; 2.

ProDom; PD002078; Fib collagen_C; 1

SMART; SM00308; COLFI; 1.

SMART; SM00282; LamG; 1.

SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                 Q25582
Q25582;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
                                                                               Teladorsagia circumcincta.
Eukaryota; Metazoa; Nemato
Trichostrongyloidea; Haemo
                                                                                                                                                                 Cuticular collagen. COLOST-1.
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NCBI_TaxID=9031;
           SEQUENCE FROM N.A.
                                                     NCBI_TaxID=45464;
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                                                                                     Nematoda; Chron; Haemonchidae;
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25.7%; Pred. No.
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MEDLINE=20068042; PubMed=10601735;

MEDLINE=20068042; PubMed=10601735;

Gordon M.K., Marchant J.K., Foley J.W., Igoe F., Gibney E.P.,

Gordon M.K., Marchant J.K., Foley J.W., Igoe F., Diblet B.,

Nah H.D., Barembaum M., Myers J.C., Rodriguez E., Diblet B.,

van der Rest M., Linsenmayer T.F., Upholt W.B., Birk D.E.;

"Complete primary structure of the chicken alpha1(V) collagen chain.";

"Matrix Biol. 18:481-486(1999).

"Matrix Biol. 18:481-486(1999).

EMBL; AF137273; AAF28099.1; -.

InterPro; IPR000087; Collagen.

InterPro; IPR000885; Fib collagen.

InterPro; IPR001230; Prenyl_site.

InterPro; IPR001230; Prenyl_site.

InterPro; IPR001230; TSPN.
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Chromadorea; Rhabditida; Stron
idae; Ostertagiinae; Teladorsag
                                                                                                                                                sequence update)
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Best Local Similarity
                                                                                                    SEQUENCE FROM N.A.
MEDLINE-97039674; PubMed=8885226;
Johnstone I.L. Shafi Y., Mjaeed A.
"Cuticular collagen genes from the
circumcincta.";
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SEQUENCE
                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Ostertagiinae; Teladorsagia.
NCBI_TaxID=45464;
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01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Mol. Blochem. Parasitol. 103:171-181(1999).
EMBL, X96731, CAR65506.1; -
                        InterPro; IPR000087; Collagen.
InterPro; IPR007486; Col cuticle_N.
Pfam; PF01391; Collagen; 3.
Pfam; PF01484; Col_cuticle_N; 1.
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01-NOV-1996
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InterPro; IPR002486; Col_cuticle_N.
Pfam; PF01391; Collagen; 3.
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Johnstone I.L., Shafi Y., Mjaeed A., Barry J.D.;
"Cuticular collagen genes from the parasitic nematode Ostertagis
 SEQUENCE
                                                                            Mol. Biochem. Parasitol. 80:103-112(1996) EMBL; X96732; CAA65507.1; -.
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Pred. No. 0.0033;
5; Mismatches 86
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Best Local S
Matches 61
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Best Local :
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01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 31.3 kDa protein.
T15B7.3.
                                                                                                                                                                                                                                                                                                                                                                                                                           "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; AF022985; AAB69959.1; -.
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                                                                                                                                                                                                                                                                                                                         InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col_cuticle_N.
Pfam; PF01391; Collagen; 3.
Pfam; PF01484; Col_cuticle_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                  Hypothetical protein
SEQUENCE 319 AA; :
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STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pauley A., Gattung S.; "The sequence of C. elsubmitted (SEP-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
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59
                                                                                                                                      13 VGALLILGVLGLVSGLSL-----EPVYWNSANKRFQAEGG----YVLYPQIGDRLDLLC
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                                            PRARPPGPHSSPNYEFYKLYLVG------GAQGRRCEA-PPAPNLLLTCDRPDLDL 111
                                                                                             MSASTLVTVASAASGIAIVVCVFTVGMIFNDINSFYDEKIGELKEFKGYEQIA--WQAMI
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FLLGRNKRQAECNCGEQSRGCPAGPPGPP-----GQPG---
                                                                                                                                                                                  ; Score 141; DB; Pred. No. 0.00 27; Mismatches
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EMBL/GenBank/DDBJ
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Pred. No. 0.
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                                                                                                                                                                                       Indels 124;
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                                                                                                                                                                                                                           Query Match
Best Local
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EMBL; AB008373; BAA33380.1; -.
InterPro; IPR000087; Collagen.
InterPro; IPR000085; Fib collagen.C.
Pfam; PF01410; COLFF; 1.
Pfam; PF01410; COLFF; 1.
ProDom; PD000007; Collagen; 9.
ProDom; PD000007; Collagen; 1.
ProDom; PD000007; Collagen; 1.
ProDom; PD000007; Collagen; 1.
ProDom; PM000038; COLFF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha 1 type I collagen (Fragment).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii; Salmoniformes, Salmonidae, Oncorhynchus.
NCBI_TaxID=8022;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                Collagen.
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258
                                                    204
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                                                                                                                                                            98
                         LGIALRGG--GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
                                                                                                                                 HSLEPGKENLPGDPTSNAT-----SRGAEGPLPPPSMPAVAGAAGGLALLL
                                                                                                                                                         ADGAGGKDGVRGMTGPIGPNGPAGSPGDK----GETGAPGAVGPSGARGAPGERGESGA
                                                                                                                                                                                    ATSDGTREGLESLOG-----GVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGA
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TGPAGRPGELGAAGPP----
                                                                             LGVAGAGGAMCWRRRRAKPSESRHPG-----PGSFGRGGSLGLGGGGGMGPREAEPGE
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                                                                                                                                                                                                                61;
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                                                                                                      PGPAGFAGPPGGDGQPGAKGEAGDNGAKGDGGAQGPAGPTGAPGPQGPAGN-----
                                                                                                                                                                                                                                                                  809
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                                                                                                                                                                                                                                                                 78164 MW;
                                                                                                                                                                                                                     7.6%;
27.4%;
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-GPKGEKGQPGGDGPNGPSGTP
                                                                                                                                                                                                              15;
                                                                                                                                                                                                            Score 141; DB
Pred. No. 0.011
15; Mismatches
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                                                                                                                                                                                                                                                                  68C056A7640FCA81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aoki T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishida M.,
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RESULT 41

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RESULT 42
Q90YC5
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01410; COLPI; 1.—
Pfam; PF01391; Collagen; 18.
Pfam; PF01093; Ywc; 1
Probom; PD000007; Collagen; 2.
Probom; PD002078; Fib collagen_C; 1.
PROSITE; PS01208; YWFC; UNKOWN 1.
PROSITE; PS01208; YWFC; UNKOWN 1.
SEQUENCE 1449 AA; 137117 MW; 62E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0910C0

0910C0

01-DEC-2001 (TrE

01-DEC-2001 (TrE

01-JUN-2002 (TrE

Collagen al(I)

COLIAI.
[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21412237; PubMed=11520665;
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
"Identification of ephrin-A3 and novel genes specific to the
"Identification of ephrin-A3 and novel differential display.";
in embryonic zebrafish by ordered differential display.";
                                                                                                                                                                                             Q90YC5;
Q90YC5;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                   #racnydanio rerio (Zebrafish)
Bukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
NCBI_TaxID=7955;
[11]
                                                                                                                                                                      EPHRIN-A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncorhynchus mykiss (Rainbow trout) (Salmo gairdner: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii, Nepopterygii; Teleostei; Euteleostei Protacanthopterygii; Salmoniformes; Salmonidae; Onco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete primary structure of rainbow trout t consisting of al(I)a2(I)a3(I) heterotrimers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21257802; PubMed=11358497;
Saito M., Takenouchi Y., Kunisaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                              868
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                                                                                                                                                                                                                                                                                                             TGPAGRPGELGAAGPP----GPKGEKGQPGGDGPNGPSGTP
                                                                                                                                                                                                                                                                                                                                      TGIATEG--GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP
                                                                                                                                                                                                                                                                                                                                                                                       LGVAGAGGAMCWRRRRAKPSESRHPG-----PGSFGRGGSLGLGGGGGMGPREAEPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                       HSLEPGKENLPGDPTSNAT------SRGAEGPLPPPSMPAVAGAAGGLALLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADGAGGKDGVRGMTGPIGPNGPAGSPGDK-----GETGAPGAVGPSGARGAPGERGESGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATSDGTREGLESLQG-----GVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
                                                                                                                                                                                                                                                                                                                                                                TGAKGARGA
                                                                                                                                                                                                                                                                                                                                                                                                                 ----PGPAGFAGPPGGDGQPGAKGEAGDNGAKGDGGAQGPAGPTGAPGPQGPAGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB052835; BAB55661.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000087; Collagen.
IPR000885; Fib collagen_C.
IPR001007; VWF_C.
                                                                                                                                                                                              (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 19, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                ----AGPPGATGFPGAAGRFGPPGPSGNNGPPGTPGPGGKEGQKGNRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268:2817-2827(2001).
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19,
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                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 141; DB Pred. No. 0.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                           (Zebra danio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62EEF8A7BFD652B8 CRC64;
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ow trout
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
                                               midbrain-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT
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Query Match 7.6%; S
Best Local Similarity 25.8%; P
Matches 69; Conservative 22;
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Best Local
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P91274;
01-MAY-1997
                                                                                                                        "Direct Submission.";
"Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
SMBL; U80444; AAB37788.1; -.
InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col cuticle_N.
Pfam; PP01391; Collagen; 2.
Pfam; PP01391; Collagen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; UNKNOWN 1.
SEQUENCE 219 AA; 25146 MW; 7191927E03F8EA01
                                                                                             Hypothetical SEQUENCE 3
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a pinvestigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mech. Dev. 107:83-96(2001).
EMBL; AB051678; BAB55891.1;
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BRISTOL N2;
MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical 30.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhabditidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179
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305 AA; :
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(TrEMBLrel. 03, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
1 30.8 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                          30770 MW;
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26.9%; Pred. No. 0.00
cive 27; Mismatches
Score 140.5;
Pred. No. 0.00
22; Mismatches
                                                                                             6BDC3ADD3E90A358
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                                         DB 5;
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  Indels
                                            Length
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  ; eB
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Matches
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01-NOV-1999
01-NOV-1999
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Pfam;
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01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
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    LGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSG
                                                                                          AVAGAAG--GLALLLLGVAGAGGAMCWRRRAKPSESRHP-----
                                                                                                                                       CEPITPPPCKPCPQGPAGAPGAPGPQGDAGAPGAP-GQGSGAGAPGPAGPKGASGAPGNP
                                                                                                                                                                                    RKPVSEMPM----ERDRGAAHSLEP-GKENLPGDPTSNATSRGAEGPLPP-----PSMP
                                                                                                                                                                                                                               EGVDQGSEGAQGGSCSGCCLPGAAGPAGTPG-----KPGRPGRPGAAGLPGNPGRPPAQP
                                                                                                                                                                                                                                                                       DGTREGLESLQGGVCL------TRGMKVLLRVGQSPRGGAV----
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Pro; IPR002486; Col cuticle_N.
PF01391; Collagen; 2.
PF01484; Col cuticle_N; 1.
                                                                                                                                                                                                                                                                                                                    59;
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                                                                                                                                                                                                                                                                                                                    Conservative
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                  Score 140; DB
Pred. No. 0.00
L6; Mismatches
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254

PSGAPGQPGADGNPGAPGQPGQAGGAGEKGICPKYCAIDG

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RESULT 46
Q9YIB4
ID Q9YIE
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Best Local S
Matches 96
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Collagen pro alpha-chain precursor.
HDCOL 1 ALPHA.
Haltoria ...
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097405;
01-MAY-1999
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Eur. J. Biochem. 261:714-721(1999).
EMBL; AB017600; BAA75668.1; -.
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MEDLINE=99234051; PubMed=10215888;
Yoneda C., Hirayama Y., Nakaya M.,
    Q9YIB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
Haliotidae; Haliotis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPHSGPGGVR--VGALLLLGVLGLVSGLSLEPVYWN--SANKRFQAEGGYVLYPQIGDR 57
                                                                                                                                             KVSGDYGHPVYIVQDGPP 330
                                                                                                                                                                                                                                                                                                                                               GOTGSDGKDGAKGDTGARGYPGEAGPIGAPGNEGREGRKGSRGSGGIPGNSGTPGDPGRA 819
                                                                                                                                                                                                                                                                                                                                                                                          LRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTR--EGLESLQGGVCLTRGMKVL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDLLCPRARP------PGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPHLLLTCDR 106
                                                                                                       GLRGDNGNDGAPGQAGPP
                                                                                                                                                                                      MPGLDGAQGERGSPGLNGPSGPPGPVGPQGERGANGFPGSQGEA----GAAGPPGSAGEP
                                                                                                                                                                                                                           ----PGSFGRGGSLGLGGGGG----MGPR-----EAEPGELGIALRGGGAADPPFCPHYE
                                                                                                                                                                                                                                                                    GPPGSPGAQGP-----PGPSGAT-----GLSGDGGE---RGETGPPGRSGEPGAPG
                                                                                                                                                                                                                                                                                                        SNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRAKPSESRHPG---
                                                                                                                                                                                                                                                                                                                                                                                                                            -----GEPGP------PGSSGQRGPAGAQGPQGPTGLSGPTGEM
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l Similarity 25.4%;
96; Conservative 2
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1378 AA;
    PRELIMINARY;
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132583 MW; 6EEE34A65B52E634 CRC64;
                                                                                                     936
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    PRT;
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    1450
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RESULT 47
Q9UMG6
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Best Local :
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InterPro; IPR001087; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
Pfam; PF01410; COLUFI; 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD002007; Collagen; 1.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM000214; VWC; 1.
Q9UMG6 PRELIMINARY;
Q9UMG6;
Q9UMG6;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 21, I
01-UUN-2002 (TrEMBLrel. 21, I
Collagen type IV a6 chain.
COL4A6.
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SEQUENCE
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Alpha 1 type I collagen.
Cynops pyrinogaser (Japanese common newt).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynop
MCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asahina K., Obara M., Yoshizato K., "Expression of genes of type I and type II collagen i and development of the blastema of regenerating newt Dev. Dyn. 216:59-71(1999).

EMBL, AB015438; BAA36973.1; ...
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                                                                                                                                                                                                                                               844 APGPKGTRGAAGPPGATGFPGAAGRLGPPGPSGNAGPPGPP 884
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M. Yoshizato K.
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Last sequence update)
Last annotation updat
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964 222

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Query Match
Best Local S
Matches 61
                                                                                                                                                                                                    Submitted (JAN-1996) to the EMBL/Ge:
EMBL U46960; AAB19039.1; JOINED.
EMBL U46961; AAB19039.1; JOINED.
EMBL U46962; AAB19039.1; JOINED.
EMBL U46963; AAB19039.1; JOINED.
EMBL U46966; AAB19039.1; JOINED.
EMBL U46966; AAB19039.1; JOINED.
EMBL U46966; AAB19039.1; JOINED.
EMBL U46966; AAB19039.1; JOINED.
EMBL U46967; AAB19039.1; JOINED.
EMBL U46977; AAB19039.1; JOINED.
EMBL U46978; AAB19039.1; JOINED.
EMBL U46979; AAB19039.1; JOINED.
EMBL U46979; AAB19039.1; JOINED.
EMBL U46979; AAB19039.1; JOINED.
EMBL U46980; AAB19039.1; JOINED.
EMBL U46981; AAB19039.1; JOINED.
EMBL U46991; AAB19039.1; JOIN
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[2]
SEQUENCE FROM N.A.
Zhang X.;
Submitted (JAN-1996
                                                                                                     ProDom; PI
SMART; SMI
Collagen.
SEQUENCE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE OF 1-1644 FROM N.A.

MEDLINE=9629942; PubMed=8661006;

Zhang X., Zhou J., Reeders S.T., Tryggvason K.;

Chang X., Zhou J., Reeders S.T. Collagen COL4A6 gene, which is mut in Alport syndrome-associated leiomyomatosis.";

Genomics 33:473-479(1996).
                                                                                                                                                             SM00111; C4;
Similarity
61; Conser
                                                                                                                                                                                F01413; C4; 2.
F01391; Collagen; 23.
PD000007; Collagen; 4.
PD003923; ProcollagnC4;
                                                                                                          1690
     Conservative
                                                                                                       AA;
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Score 139.5;
Pred. No. 0.03
25; Mismatches
                                                                                                          4698AE2CC2D3E859
                         DB 4;
                                                                                                          CRC64;
                                                  Length
                                               1690;
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Q9Y4L4;
Q9Y4L4;
01-NOV-1999 (TrEMBLrel. 12, C
01-NOV-1999 (TrEMBLrel. 21, I
01-JUN-2002 (TrEMBLrel. 21, I
Collagen type IV a6 chain.
CCL4A6.
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MEDILINE=96299642; PubMed=8661006;
Zhang X., Zhou J., Reeders S.T., Tryggvason K.;
"Structure of the human type IV collagen CCL4A6
in Alport syndrome-associated leiomyomatosis.";
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Mammalia; Eutheria;
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U46959;
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ABB19038.11
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Primates;
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AK074129; BAB84955.1; -

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RESULT 49
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AC Q8TEJ
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                     QBTEJ5;
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InterPro; IPR001442; ProcollagnC4
Pfam; PF01413; C4; 2.
Pfam; PF01391; Collagen; 23.
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                      Jikuya H., Takar
"The nucleotide
                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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  Submitted
                                                                                                                   Homo sapiens (Human).
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                                                                               NCBI_TaxID=9606;
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ISSUE=SPLEEN;
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U46987; AAB19038.1;
U46989; AAB19038.1;
U46989; AAB19038.1;
U46999; AAB19038.1;
U47000; AAB19038.1;
U47000; AAB19038.1;
U47000; AAB19038.1;
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U47000; AAB19038.1;
U47000; AAB19038.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
  (JAN-2002)
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                                  Takano
                                                                                                                                                                                                  PRELIMINARY;
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Pred. No. 0.03
25; Mismatches
 EMBL/GenBank/DDBJ databases
                                                                                          Craniata; Vertebrata; I Catarrhini; Hominidae;
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                       R., Nagase T., clone isolated
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                                                                                                       Euteleostomi;
                        Ohara
| from !
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RESULT 50
Q9D2V4
ID Q9D2V
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                                                                                                                                                                                                                                                                                                                                                              RX MEDLINE=21085660; Pubmede=11217851;
RA Arakawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno M., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno M., Adachi J., Fukuda S.,
RA Alzawa M., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Isawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Joshida M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.,
Hayashizaki Y.,
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Best Local
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NON TER
SEQUENCE
PRINTS; PRO0007; COMPLEMNTCIQ. SMART; SM00110; C1Q; 1. PROSITE; PRO1113; C1Q; 1. SEQUENCE 744 AA; 73581 MW;
                                                                                 InterPro; IPR001073; C1q.
InterPro; IPR001073; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 7.
PRINTS; PR00007; COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9D2V4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Procollagen,
COL8A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, C:
01-JUN-2001 (TrEMBLrel. 17, L:
01-JUN-2001 (TrEMBLrel. 17, L:
Procollagen, type VIII, alpha
                                                                                                                                                                                                                                                  EMBL; AK018742; BAB31383.1; MGD; MGI:88463; Col8a1.
                                                                                                                                                                                                                                                                                                                Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKVSGDYGHPVYIVQDGP-----PQSPPNI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGLKGDNGVGQPGLPGAPGQGGAPGPP---GLP----GPAGLGKPGLDGLPGAPGDKGES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -Sesrhpgp-gsfgregsleigeggggmgpreaepgelgialrgggaadppfcphy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%;
31.4%;
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Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
   C659BDCCBCD6EB9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07DB85A65A948ED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            744
                                                                                                                                                                                                                                                                                                                                              mouse cDNA collection.";
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Sear	皮	Ş	皮	Ş	В	Ş	뭥	Ś	Вb	ş	В	Ą	Que
th cor	445	296	389	253	334	211	274	169	235	115	199	67	Query Match Best Local Matches 8
Search completed: February 11, 2003, 12:05:05	GEVGPPGMRGLPGPIGPKGEGHKGLPGLPGVPGLLGPKGEP-GIPGDQGLQGPPGI 500	ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNI 336	PPGEPGLPGIPGPMGPPGAIGFPGPKGEGGVVGPQGPPGPKGEPGLQGFPGKPGFL 444	RRRAKPSESRHPG-PGSFGRGGSLGLGGGGGMGPREAEPGELGI 295	KGEQGLPGLPGPEGLPGVGKPGFPGPKGDRGIGGVPGVLGPRGEKGPIGAPGMGG 388	ATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWR 252	KPGVTGFPGGPQGELGKPGPPGBPGPQGLIGVPGVPGVPGVPGKPGQDGIPGQPGFPGG 333	QSPRGGAVPRKEVSEMEMERDRGAAHSLEEGKENLEGDETSN 210	PGLQGPKGEKGFGMPGLPGLKGPPGMHGPPGPVGLPGVG 273	IKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVG 168	PPGPHGLPGIGKPGGPGLPGQPGAKGERGPKGPPGP 234	PPGPHSSPNYEFYKLYLVGGAQGRR-CEAPPAPNLLLTCDRPDLDLRFT 114	Query Match 7.5%; Score 139; DB 11; Length 744; Best Local Similarity 23.2%; Pred. No. 0.014; Matches 83; Conservative 28; Mismatches 104; Indels 142; Gaps 18;

Search completed: February 11, 2003, 12:05:05 Job time : 36.2327 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum DB seq length: 200000000
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         333008
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       1850
637.5
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                                                                                                                                                                                       Last sequence update)
Last annotation update)
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EXTRACELLULAR (DOTENTIAL).
POTENTIAL.
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PDZ RECOGNITION MOTIF (POT
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R -> Q.
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Pred. No. 3.7e-113;
; Mismatches 0;
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EDFF2A23C2FDE79F CRC64;
                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                  Brambilla R.,
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"Complementary expression of transmembrane ephrins and their receptors
of in the mouse spinal cord: a possible role in constraining the
orientation of longitudinally projecting axons.";

The development 127:1397-1410(2000).

C -1- FUNCTION: WAY PLAY A PILYOTAL ROLE IN FOREBRAIN FUNCTION. BINDS TO,
AND INDUCE THE COLLAPSE OF, COMMISSURAL AXONS/GROWTH CONES IN
C -1- FUNCTION: WAY PLAY A ROLE IN CONSTRAINING THE ORIENTATION OF
LONGITUDINALLY PROJECTING AXONS.

C -1- SUBCELLULAR LOCATION: Type I membrane protein.
C -1- SUBCELLULAR LOCATION: Type I membrane protein.
C -1- SUBCELLULAR LOCATION: Type I membrane protein.
C SPECIFICALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROUGH
THE FLOOR PLATE. EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL
C LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISC.

-1- DEVELOPMENTAL STAGE: EXPRESSED IN THE FLOOR PLATE THROUGHOUT THE
PERIOD OF COMMISSURAL AXON PATHFINDING.

-1- SIMILARITY; BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF025288; AAC53537.1; -. MGD; MGI:109196; Efnb3. InterPro; IPR001799; Ephrin.
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GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEFGELGIALRGG
                                                                          VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPEPSMPAVAGAAGGMALLLL
                                                                                                                                                                                                                  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
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                                                                                                            VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL
                                                                                                                                                                              SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP
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PD002533; Ephrin; 1.
PS01299; EPHRIN; 1.
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ilarity 95.6%;
Conservative
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Pred. No. 1.2e
7; Mismatches
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PDZ RECOGNITION MOTIF (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
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hes 8;
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                                                                         "Complementary expression of transmembrane ephrins and their receptors
or in the mouse spinal cord; a possible role in constraining the
orientation of longitudinally projecting axons.";

Development 127:1397-1410(2000).

1- FUNCTION: MAY PLAY A ROLE IN CONSTRAINING THE ORIENTATION OF
C- PUNCTION: MAY PLAY A ROLE IN CONSTRAINING THE ORIENTATION OF
C- ISUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASE EPHB4.

1- SUBCELLULAR LOCATION: Type I membrane protein.
C- I- SUBCELLULAR LOCAMISSURAL AXON SECRENTS THAT HAVE PASSED THROUGH
THE FLOOR PLAYE. EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL
C- LAYER DURING RETINAL AXON GUIDANCE TO THE OPIC: DISC:
C- DEVELOPMENTAL STAGE: EXPRESSED IN THE FLOOR PLAYE THROUGHOUT THE
DERIOD OF COMMISSURAL AXON PATHFINDING.
C- I- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE
C CYTOPLASMIC DOWAIN (BY SIMILARITY).
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P52906 (Rel. 34, Last sequence update)
P52002 (Rel. 34, Last annotation update)
P52002 (Rel. 34, Last annotation update)
P52002 (Rel. 34, Last annotation update)
P52002 (Rel. 34, Last annotation update)
P52002 (Rel. 34, Last annotation update)
P52002 (Rel. 34, Created)
P52002 (Rel. 34, Last sequence update)
P52002 (Rel. 34, Last seq
                     This SWI
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Cerretti D.P., Vanden Bos T., Nelson N., Kozlosk
Maraskovsky E., Park L.S., Lyman S.D., Copeland
Gilbert D.J., Jenkins N.A., Fletcher R.A.;
"Isolation of LERK-5: a ligand of the eph-relate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95199254; PubMed=7534404;
Bennett B.D., Zeigler F.C., Gu Q., Fend
Gillett N., Matthews W.;
"Molecular cloning of a ligand for the
tyrosine kinase Htk.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bergemann A.D., Cheng H.J., Brambilla R., Klein R., Flanagan J.G.; "ELF-2, a new member of the Eph ligand family, is segmentally expressed in mouse embryos in the region of the hindbrain and newless
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Mol. Cell. Biol, 15:4921-4929(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ICR; TISSUE=Brain;
MEDLINE=95379837; PubMed=7651410;
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STRAIN=CBS7BL/6J X SJL/J;
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Mammalia; Eutheria;
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                                          SWISS-PROT
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ROT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its
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Sciurognathi; Muridae;
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                                   NCBI_TaxID=9606;
                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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      FROM N.A.
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FFB1 HUMAN

199172;

01-OCT-1996 (Rel. 34, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Finin'Bl precursor (EPH-related receptor tyrosine

Finin'Bl precursor (EPH-related receptor tyrosine)

Finin'Bl precursor (EPH-related receptor tyrosine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U16819; AAA99708.1; -.
EMBL; L38847; AAC42052.1; -.
EMBL; U30244; AAA82934.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U30244; AAA82934
MGD; MGI:105097; Efnb2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF0081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 GALLLIGVIGLYSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS
                                                                                                                                                                                                                                                                                                                                                    WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGGGAADPPFFCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH
                                                                                                                                                                                                                                                                                                                                                                                         GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                           GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV
                                                                                                                                                                                                                                           YEKVSGDYGHÞVYÍVQEMÞÞQSÞANÍYYKV
                                                                                                                                                                                                                                                                              YEKVSGDYGHPVYI VQDGPPQSPPNI YYKV
                                                                                                                                                                                                                                                                                                                 KYRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Neurogenesis; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephrin; 1
17; EPHRIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 637.5;
Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
MISSING (IN REF. 3).
A -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL)
PDZ RECOGNITION MOTIF (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPHRIN-B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D08894996E399554 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Bi
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Primates;

Chordata;

Craniata; Vertebrata; Euteleostomi;

kinase ligand

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                                   S
                                                                                                                      Query Match
Best Local Sin
Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Fletcher F.A., Huebner K
Kozlosky C., Druck T., S
Cerretti D.P., Belmont J
Submitted (JAN-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Davis S., Gale N.W.,
Pawson T., Goldfarb M
Submitted (NOV-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE
                                                                                                                   CARBOHYD
SEQUENCE
                                                                                                                                               DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                  Signal SIGNAL
                                                                                                                                                                                                                                                                                                                                                 EMBL; U09304; AAA53093.1; -.
EMBL; L37361; AAA52369.1; -.
EMBL; U09303; AAB41127.1; -.
EMBL; AL136092; CAB86409.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING TO RIENTARION OF LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY)

-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB1 AND EPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta;
MEDLINE=94349923; PubMed=8070404;
Beckmann M.P., Cerretti D.P., Baum P., Vandenbos T., Ja
Farrah T., Kozlosky C., Hollingsworth T., Shilling H.,
Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;
"Molecular characterization of a family of ligands for
tyrosine kinase receptors.";
EMBO J. 13:3757-3762(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                    PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (se or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                          Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Howden
                                                                                                                                                                                                                                                                                                            InterPro; IPR001799; Ephrin.
            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDS GRIP1 AND GRIP2.
SUBCELLULAR LOCATION: Type I membrane
TISSUE SPECIFICITY: HEART, PLACENTA, L
KIDNEY, PANCREAS.
INDUCTION: BY TNF-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: INDUCIBLE PHOSPHORYLATION OF TYROSIN CYTOPLASMIC DOMAIN (BY SIMILARITY). SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European
                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way field and this statement is not removed. Usage by and for commercial.
                                                                                                                                                                                                                                                                                                                          300035
            PGQRWLGKWLVAMVVWALCRLATPLAKNĹEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
                                     PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL
                                                                                                                                                                                                                                                                                              PF00812; Ephrin
                                                                                                                                                                                                                                                                                                                                      HGNC: 3226;
                                                                              Similarity
                                                                                                                                                                                                                             Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                   protein; Neurogenesis;
                                                                                                                     Ã,
                                                                                                            224
2346
237
2346
3346
339
                                                                                                                                                                                                                                                                                                                                       EFNB1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             er K., Shaffer L.G., Monaco A., Mue

'., Simoneaux D.K., Fairweather N.,

nt J.W., Beckmann M.P., Lyman S.D.,

to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aldrich T.H., Maisonpierre P.C., M., Yancopoulos G.D.; to the EMBL/GenBank/DDBJ databas
                                                                             34.2%;
                                                                                                                      ₹
                                                                                                                POTENTIAL.

EMPACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

PDZ RECOGNITION MOTIF (POTENTIAL).

N-LINKED (GLCKAC. . .) (POTENTIAL).

M, 473DDZF1A5BF89DE CRC64;
                                                                48;
                                                              Score 632; DB
Pred. No. 2.5e
8; Mismatches
                                                                                                                                                                                                                                          Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             le protein.
LUNG, LIV
                                                                             DB 1;
.5e-34;
                                                                 116;
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                                                                                           Length
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S.D.;
                                                                Indels
                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 James L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lhotak
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin-B2 precursor (EPH-related receptor to (LERK-5) (HTK ligand) (HTK-L).
EFNB2 OR EPLG5 OR LERK5 OR HTKL.
melanomas.";

Clin. Cancer Res. 4:791-797(1998).

Clin. Cancer Res. 4:791-797(1998).

I CONSTRAINING THE OF ILONGITUDINALLY PROJECTING AXONS (BY SIMILARITY).

LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY).

SUBURILY BINDS TO THE RECEPTOR TYROSINE KINASES.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: LUNG AND KIDNEY.
                                                                                                                                                                                                                                                                                                                  "Isolation
kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=98192220; PubMed=9533549;
Vogt T., Stolz W., Welsh J., Jung
                                                                                                                                                                                                                       Bennett B.D., Zeigler F.C.,
Gillett N., Matthews W.;
                                                                                                                                                                                                                                                                                                                                             MEDLINE=96145238, PubMed=8559144;
Cerretti D.P., Vanden Bos T., Nelson N
Maraskovsky E., Park L.S., Lyman S.D.,
Jenkins N.A., Fletcher R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFB2_HUMAN
P52799;
                                                                                        Vogt T., Stolz W. Welsh J., Jung B., Kerbel R.S.,
Landthaler M., McClelland M.;
"Overexpression of Lerk-5/Eplg5 messenger RNA: a I
increased tumorigenicity and metastatic potential
                                                                                                                                                                                 "Molecular cloning of a ligand
tyrosine kinase Htk.";
Proc. Natl. Acad. Sci. U.S.A. 9
                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=95199254;
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM 
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVFRKPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----
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                                                                                                                                                                                                                                                                                                                                  LERK-5:
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                                                                                                                                                                                                                                   PubMed=7534404;
qler F.C., Gu Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS
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                                                                                                                                                                                                                                                                                                                               ligand of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata;
Catarrhini; Hominidae
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073612;
15-JUL-1999
15-JUL-1999
16-OCT-2001
              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin-B1 precursor (CEK5 ligand) (CEL5-L).
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SEQUENCE
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SIGNAL
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-i- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
   Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
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PRINTS; PR01347; EPHRIN.
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PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
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Dev. Biol. 182:556-269(1997).
-i- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASE EPHB2.
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- STMCLILLE PHOSPHORYLATION OF TYROSINE RESIDUES IN CYTOPLASMIC DOMAIN (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01347; EPHRIN.
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MEDLINE=97223524; PubMed=9070326;
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                                       GSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQS
                                                                                    GLEFKRQQDYFITSTSNGTLDGLENREGGVCQTRSMKIVMKVGQDP-NAVIPEQLTTSRP
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-BPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQBMPPQS
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

PDZ RECONITION MOTIF (POTE

PDZ RECONITION MOTIF (POTE

N'LINKED (GLONAC...) (POT
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Pred. No. 4.4e-34;
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Best Local
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DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes Dev. 12:3096-3109(1998).

-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASE EPHB4.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES I
CYTOPLASMIC DOMAIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98438455, PubMed=9765210;
MEDLINE=98438455, PubMed=9765210;
Durbin L., Brennan C., Shiomi K., Cooke J.,
Shanmugalingam S., Guthrie B., Lindberg R.,
"Eph signaling is required for segmentation
"Eph signaling is required for segmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ004863; CAA06168.1; -. ZFIN; ZDB-GENE-990415-67; efnb
InterPro; IPR001799; Ephrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Developmental protein; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                Prodom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00812; Ephrin;
PRINTS; PR01347; EPHRI
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15-JUL-1999 (Rel. 38, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
              193
                                             128
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                AHS--
                                             DYYIISTSNGTMEGLDNQEGGVCKTKSMKIIMKVGQNPSDPISPKDYPTSYPPKHPDLGG
                                                                    DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK-PVSEMPMERDRGA
                                                                                                        EGVEYYKLYMVPLEQLKSCQVTKADTPLLNCVKPDQDVKFTLKFQEFSPNLWGLEFFRGK 127
                                                                                                                                       PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 13:
                                                                                                                                                                   GVLVIACKVNLSRALILDSIYWNTTNTKFVPGQGLVLYPQIGDKMDIVCPRVE---GGSM
                                                                                                                                                                                                                                                Similarity
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225 H
246 P
332 C
332 C
36724 WW;
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              GKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGV
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
PDZ RECOGNITION MOTIF (POT.
PDZ RECOGNITION MOTIF (POT.
N; 189ED82372C71C8B CRC64;
                                                                                                                                                                                                                              Score 626.5; DB 1
Pred. No. 5.4e-34;
4; Mismatches 106
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Holder N.;
and differentiation
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RX MEDLINE=20171264; PubMed=10704386;
RA IMONDAL R., Wideman C., Kaprielian Z.;
IMONDAL R., Wideman C., Kaprielian Z.;
RT inchementary expression of transmembrane ephrins and their receptor in the mouse spinal cord: a possible role in constraining the rolentation of longitudinally projecting axons.";
LDEVelopment 127:1397-1410(2000).
C -!- FUNCTION - BINDS TO, AND INDUCE THE COLLARSE OF, COMMISSURAL AXONS/GROWTH CONCES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE COLENTATION OF LONGITUDINALLY PROJECTING AXONS.
C -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB1 AND EPHA1 ---
-!- TISSUE SPECIFICATION: Type I membrane protein.
SPECIFICALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROI THE FLOOR PLATE. EXPRESSED ON CELLS OPTIC BISC.
-!- TURKER DURING RETURAL AXON GUIDANCE TO THE OPTIC DISC.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE FLOOR PLATE THROUGHOUT THE PERIOD OF COMMISSURAL AXON PATHFINDING
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P52795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene encoding
elk.";
                                                                                                                                                                                                                                                                                                                       MEDLINE=95014510; PubMed=7929389;
Shao H., Lou L., Pandey A., Pasquale
"CDNA cloning and characterization of
protein-tyrosine kinase.";
J. Biol. Chem. 269:26606-26609(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fletcher F.A., Renshaw B., Hollingsworth T., Baum P., Lyman S.D., Jenkins N.A., Gilbert D.J., Copeland N.G., Davison B.L.; "Genomic organization and chromosomal localization of mouse Eplggene encoding a binding protein for the receptor tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01.0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-Bl precursor (EPH-related receptor tyrosine
(LERK-2) (ELK ligand) (ELK-L) (STRA1 protein) (CEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel.
01-OCT-1996 (Rel.
30-MAY-2000 (Rel.
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of a ligand
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or the Cek5 receptor
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receptor ligand)
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kinase ligand

Euteleostomi;
; Murinae; Rattus.

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RESULT 9
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ID EFB1_RAT
AC P52796;
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Best Local Sin
Matches 138;
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EMBL; U07598; AAC53247.1; JOINED.
EMBL; U07599; AAC53247.1; JOINED.
EMBL; U07509; AAC53247.1; JOINED.
EMBL; U17600; AAC53247.1; JOINED.
EMBL; Z48781; CAA88695.1; -.
EMBL; U12983; AAA53231.1; -.
MGD; MGG:102708; EERBL.
TENTONOS; EERBL.
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CONFLICT
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Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PB002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
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DOMAIN
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                HDYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA 192
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                                                                                                                                                                                                     VALFAAVGAGCVIFLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSLSTLASP
                                                                                                                                                                                                                                                                VKT-----ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGDSDSFFNSK
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               STANDARD;
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239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.

CYTOPLASMIC (POTENTIAL).

PDZ RECOGNITION MOTIF (POTENTIAL).

PDZ RECOGNITION MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 613.5;
Pred. No. 3.9
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EXTRACELLULAR (POTENTIAL).
               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> T (IN REF. 2).
8C96FD3DC5CBC405 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 107;
               345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 1;
                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
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Best Local
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TRANSMEM
DOMAIN
DOMAIN
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Fletcher F.A., Carpenter M., Shilling H., Baum P., Ziegler S.,
Gimpel S., Hollingsworth T., Vandenbos T., Davison B.L.,
Lyman S.D., Beckmann M.P.;
"LERK-2, a binding protein for the receptor-tyrosine kinase ELK, is
evolutionarily conserved and expressed in a developmentally regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-Bl precursor (EPH-related receptor tyrosine (LERK-2) (ELK ligand) (ELK-L).
EFNBI OR EFIG2 OR LERKZ.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U07560; AAA53092.1; -. InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                              Developmental protein; Neurogenesis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF0081
                               130
   193
                                                                                                                    73
                                                                                                                                                15
                                                                                                                                                                           15 ALLLIGVIGIVSGI--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPHB1 AND EPHB2.
SUBCELLULAR LOCATION: Type I membrane protein.
STR. INDUCTBLE PHOSPHORYLATION OF TYROSINE RESIDUES
CYTOPLASMIC DOMAIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL AXONS/GROWTH CONES IN VITRO. WAY PLAY A ROLE IN CONSTRAINING TO CRIENTATION OF LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY) SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB3 (PREFERE
                                                                                                        AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP--
 AHSLEPGKENLPGDPTSNATSRGAEGP---
                                                        HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA
                                                                                       ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKEQQEIRFTIKFQEFSPNYMGLEFKKY
                               HDYYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT
                                                                                                                                                                                                       al Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation.
                                                                                                                                                                                                                                                                  345
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                  A.
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                                                                                                                                                                                                                                                                37951 MW;
                                                                                                                                                                                                                      38.0%;
                                                                                                                                                                                                       52;
                                                                                                                                                                                                                   Score 608.5;
Pred. No. 8.2
                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
PDZ RECGANITION MOTIF (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL);
1 1B3045C5C7358F7E CRC64;
                                                                                                                                                                                                                                                                                                          EPHRIN-B1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Sciurognathi; Muridae;
                                                                                                                                                                                                        Mismatches
   -LPPPSMPAVAGAAGG--
                                                                                                                                                                                                                     .2e-33;
                                                                                                                                                                                                                                   DB 1;
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Indels Length

65;

Gaps

10;

72 72

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236 188 192 129

345;

Glycoprotein;

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HHE

(PREFERRED)

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EPSILT 10
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ID EFSILX
AC 013097
AC 01-007
DT 01-NOV
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                                                CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burppean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones T.L., Karavanova I., Chong L., Zhou R.P., Daar I.O.; "Identification of XLerk, an Eph family ligand regulated during mesoderm induction and neurogenesis in Xenopus laevis."; Oncogene 14:2159-2166(1997).

-!- FUNCTION: MAY HAVE A ROLE IN THE DEVELOPING MESENCHYMAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-Bl precursor (EPH-related receptor tyrosine kinase ligand (LERK-2) (ELK ligand) (ELK-L) (XLERK).
                                                                                                                                                             TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                               CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97316777; PubMed=9174051;
                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00812; Ephrin; PRINTS; PR01347; EPHRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U31427; AAC35995.1; -. InterPro; IPR001799; Ephrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NERVOUS TISSUE.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: IN THE ADULT, EXPRESSED AT LOW LEVELS IN

TISSUE SPECIFICITY: IN THE ADULT, EXPRESSED AT LOW LEVELS IN

ADULT TISSUES WITH INCREASED LEVELS OBSERVED IN THE KIDNEY,

OCCYTES, OVARY AND TESTIS.

PYM: INDUCIBLE PROSPHORYLATION OF TYROSINE RESIDUES IN THE

CYTOPLASMIC DOMAIN (BY SIMILARITY).

SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                            mental protein; Neurogenesis; Transmembrane; Phosphorylation.
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                                                                                         327
327
327
327
327
131
                                                        ₹
.
                                                                                CYTOFLASMIC (POTENTIAL).

PDZ RECOGNITION MOTIF (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                               EPHRIN-B1.
EXTRACELLULAR
                                                    71230CE7F6BE5974 CRC64;
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                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi
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RESULT 11
EFA2_BRARE
ID EFA2_B
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Best Local Sim
Matches 146;
                                                                                                                                                                                                                                                                                                           Actinopterygii; Neopterygii; T
Cyprinidae; Danio
                                                                                                                                                                                                                                                                                                                                                               TEFA2_BRARE STANDARD; PRT; 195 AA.
179727;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyrosine
(LERK-6) (ELF-1) (ZFEPHI3).
EFNA2 OR EFIG6 OR LERK6.
                                 -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDERAIN OF DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT I EXPRESSED THROUGHOUT THE MIDERAIN INCLUDING THE REGION OF THE PRESUMPTIVE TECTUM. AT LATER STAGES IT IS EXPRESSED IN A GRADE FASHION THROUGHOUT THE TECTUM.
                                                                                                                                                                                                                         MEDLINE=97195707; PubMed=9043080;
Brennan C., Monschau B., Lindberg R.,
Bonhoeffer F., Holder N.;
                                                                                                                                     -!- FUNCTION: CONTROL AXON
OF THE RETINO-TECTAL N
-!- SUBCELLULAR LOCATION:
                                                                                                                                                                         zebrafish.";
Development 124:655-664(1997)
                                                                                                                                                                                                  "Two Eph receptor tyrosine kinase ligands control be involved in the creation of the retinotectal ma
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                       Brachydanio
                                                                                                                                                             -!- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIRRILGILLVLYRLCSALGKNIEPVTWNSQNPRFISGKGLVLYPBIGDRIDIICPKGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVR--VGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLEFRRNQDYYITSTSNSTLQGLENREGGVCQTRSMKIIMKVGQDP--NAVPPEQLT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLW 125
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                                                                                                                                                                                                                                                                                                                                                       rerio
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                                                                                                                                                                                                                                                                                                                                                       (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.4%;
                                                                                                                                                                AXON
                                                                                                                                      MAP.
: Attached
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                               GROWTH
                                                                                                                                                                                                                                                                                                                              (Danio rerio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 600; DB 1;
Pred. No. 2.8e-32;
3; Mismatches 100
                                                                                                                                                             AND MAY BE INVOLVED
                                                                                                                                      to the membrane
                                                                                                                                                                                                                                      Guthrie B., Drescher U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100;
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the
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                                                                                                                                         GPI-anchor
                                                                                                                                                                 THE CREATION
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    a collaboration
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outstation

THYMUS,

PROSTATE, TESTIS,

OVARY, SMALL INTESTINE,

AND PERIPHERAL

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Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P52797;
P52797;
P52797;
P52797;
O1-OCT-1996 (Rel. 34, Created)
O1-OCT-1996 (Rel. 34, Last sequence update)
O1-OCT-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ephrin-A3 precursor (BPH-related receptor tyrosine kinase ligand (LERK-3) (EHKI ligand) (EHKI-L).
(LERK-3) (EHKI ligand) (EHKI-L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
EFA3_I
                     MEDIINE=95063919; PubMed=7973638; Davis S., Gale N.W., Aldrich T.H., Maisonpierre Pawson T., Goldfard M., Yancopoulos G.D.; "Ligands for EPH-related receptor tyrosine kinas membrane attachment or clustering for activity." Science 266:816-819(199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001799; Ephrin.
Pfam; PP00811; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. U entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           Cerretti D.P., Beckmann M.P.;
"Ligands for the receptor tyrosine kinases
cDNAs encoding a family of proteins.";
Oncogene 10:299-306(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Hokaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mummalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                      MEDLINE=95140419; PubMed=7838529;
Kozlosky C.J., Maraskovsky E., Mc
Teepe M., Lyman S.D., Srinivasan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZFIN; ZDB-GENE-990415-66; efna2.
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                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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  SUBCELLULAR
TISSUE SPEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAPPAPNLLLTCDR---PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE 149
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  SPECIFICITY: EXPRESSED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . protein; Neurogenesis; Glycoprotein; GPI
1 16 POTENTIAL.
17 195 EPHRIN-A2.
32 N-LINKED (GLCNAC. . .) (P
5 AA; 22688 MW; 9EE284FEB61DOC42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                      ovsky E., McGrew
Srinivasan S., 1
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Pred. No. 1.2e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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  IN BRAIN,
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STRAIN=Swiss Webster; TISSUB=Brain; MEDLINE=95007776; PubMed=7522971; Cheng H.J., Flanagan J.G.; "Identification and cloning of ELF-1, ligand for the Mek4 and Sek receptor tell 79:157-168(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Buropean Bioinformatics Institute of Bioinformatics and the EMBL the Buropean Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U14187; AAC50078.1; -. EMBL; L37360; AAA52368.1; -.
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                                                                                                                              SEQUENCE FROM N.A.
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PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
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Rodentia;
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:hi; Muridae;
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Best Local S
Matches 58
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15-DEC-1998 (Rel. 37, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyr
(LERX-6) (HEK7-ligand) (HEK7-L).
EPNA2 OR EPLG6 OR LERX6.
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EMBL; U14752; AAA68520.1; -.
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                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                              152
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IGNAL
                                                                                                                                                                                                                                                                                                                                     94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            um; PF00812; Ephrin; 1.
(NTS; PR01347; EPHRIN.
)Dom; PD002533; Ephrin; 1.
)SITE; PS01299; EPHRIN; 1.
)Coprotein; GPI-anchor; Signal.
ycoprotein; GPI-anchor; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                  VYWNSANKRFQAE----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA
                                                                                                                                                                                                                          EAPEPIFTSNSSCSGLGG
                                                                                                                                                                                                                                                   GDP----TSNATSRGAEG
                                                                                                                                                                                                                                                                                                                                                            QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT
                                                                                                                                                                                                                                                                                                                                                                                        VYWNRSNPRFOVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE
                                                                                                                                                                                                                                                                              ----PNLVDRPCLR--LKVYVR
                                                                                                                                                                                                                                                                                                       REGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPWSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                                                                                                                                                                                                   GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFOLFTPFSLGFEFRPGHEYYYISATP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                 ; Metazoa; Chordata; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
EPHRIN-A2.
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 176; DB 1; I
Pred. No. 4.9e-05;
9; Mismatches 69;
                 Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .)
(GLCNAC. . .)
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                   Hominidae;
                                                                                  tyrosine
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(POTENTIAL)
                              Euteleostomi;
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EMBL; U92893; AAC39577.1; JOINED.
EMBL; U92894; AAC39577.1; JOINED.
EMBL; AC004258; AAC04896.1; -.
EMBL; AJ007292; CAA07435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aasheim H.C., Pedeutour F., Grosgeorge J., Logtenberg "Cloning, chromosal mapping, and tissue expression of encoding the human Eph-family kinase ligand ephrin-A2. Biochem. Biophys. Res. Commun. 252:378-382(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise
Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
Montomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cerretti D.P., Nelson N.; "Characterization of the genes for mouse LERK-3/Ephrin-A3 mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 conservation of intron/exon structure."; Genomics 47:131-135(1998).
                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                              ProDom; PD002533; PROSITE; PS01299;
                                                                                                                                                                                                                                                                          Pfam; PF00812; Ephrin; 1
PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                Genew; HGNC:3222; EFNA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99045414; PubMed=9826538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carrano A.V.;
Submitted (MAR-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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[1]
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                                                                                                                                                                                                                                                                                                      InterPro;
39
                         IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Attached to the membrane
                         VYWNSANKRFQA-----EGGYVLYFQIGDRLDLLCPRARPFGPHSSPNYEFYKLYLVGGA
                                                                                                                                                                                                                                                                                                                     602756;
VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PABRMEHYVLYMVNGE
                                                  ch 9.5%;
l Similarity 36.8%;
43; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                    IPR001799; Ephrin.
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213 i
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                                                                                                         A
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                                                                                                         23878 MW;
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Signal.
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                                                                                                                    POTENTIAL.

EPHRIN-A2.

N-LINKED (GLCNAC. ..)

N-LINKED (GLCNAC. ..)

N-LINKED (GLCNAC. ..)

R -> A (IN REF. 3).

RA -> PR (IN REF. 3).

AA -> RR (IN REF. 3).
                                                  Score 175.5;
Pred. No. 5.4e
L4; Mismatches
                                                                                                         33C9FB1A8168B2D0 CRC64;
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                                                    les 51;
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Interpro; IPR0017y,
Interpro; IPR0017y,
Pfam; pF00812; Ephrin; 1.

PRINTS; PR01347; EPHRIN; 1.

PRINTS; PR01299; EPHRIN; 1.

DR PROSITE; P801299; EPHRIN; 1.

20 POTENTIAL.

31 20 EPHRIN-A2.

36 N-LINKED (GLCNAC. ..) (POTENTIAL.

N-LINKED (GLCNAC. ..) (POTENTIAL.

N-LINKED (GLCNAC. ..) (POTENTIAL.

8FABIAESB45ED96 CRC64;

DB 1; Length 2'

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Matches 49
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand (LERK-6) (ELF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95360981; PubMed=7634327; Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.; Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.; "Complementary gradients in expression and binding of ELF-1 and Mek4 in development of the topographic retinotectal projection map."; Cell 82:371-381(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT ACROSS T
BEING MORE STRONGLY EXPRESSED AT THE POSTERIOR POLE
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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Gallus gallus (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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 123
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                                                                                                                               7
   FSLGFEFRPGHEYYYISAS
                                 NLWGHEFRSHHDYYIIATS
                                                              EEPLP--AERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLKFSEKFQLFTP
                                                                                              RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSP 122
                                                                                                                                 AALLAAI VG
                                                                                                                                                           ALLILGVIGLYSGISIEP------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA 65
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SEQUENCE
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ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- TISSUE SPECIFICITY: EXPRESSED IN A GRADED FASHION ACROSS THE TECTUM BEING MORE STRONGLY EXPRESSED TOWARDS THE POSTERIOR POLE -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- FUNCTION: INDUCES GROWTH COME COLLAPSE AND GANGLION CELL AXONS.
-1- SUBCELLULAR LOCATION: Attached to the membi
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Drescher U., Kremoser C., Handwerker C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFNA5 OR RAGS. [Follows]
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
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                                                             SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMP--A
-PANSCMKTIGVHDRVFDVNDKVENŠLEPADDTV---RESAEPSRG-ENAAQTPRIPIRL
                                                                                                                                                                                             FTIKFQEYSPNLWGHEFRSHHDYYIIATS---DGTREGLESLQGGVCLTRGMXVLLRVGQ 169
                                                                                                                                                                                                                                                                                                                                                                                                        MLLLAVAALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQ-QGDYHIDVCINDYLDVFCPH
                                                                                                                                  FSEKFOLFTPFSLGFEFRPGREYFYISSAIPDNGRRS-----CLK--LKVFVR---
                                                                                                                                                                                                                                                                     YEDSVPEDKT--ERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPN-----GPLK
                                                                                                                                                                                                                                                                                                                                   ARPPGPHSSPNYEFYKLYLVG------GAQGRRCEAPPAPNLLLTCDRPDLDLR 112
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228 AA;
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Pred. No. 0.00012;
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N-LINKED (GLCNAC. . .) (F
% 56D8E4FBDECF18AD CRC64;
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MBL outstation -
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PROPEP
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LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- ALTERNATIVE PRODUCTS: 2 isoforms; 1/GPI-anchored (shown he 2/secreted; are produced by alternative splicing.
-i- TISSUE SPECIFICITY: EXPRESSED IN THE ADULT SPLEEEN, LYMPH PROSTATE, OVARY, SMALL INTESTINE, AND COLON, AND IN FETALLUNG, LIVER AND KIDNEY. ALSO DETECTED IN HEMATOPOIETIC CEL-i- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blood 95:221-230(2000).
-!- FUNCTION: MAY PLAY A ROLE IN THE INTERACTION BETWEEN ACTIVATED LYMPHOCYTES AND DENDRITIC CELLS IN TONSILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
MEDILINE=95140419; PubMed=7838529;
KOZIOSKY C.J., Maraskovsky E., McGrew J.T.,
Teepe M., Lyman S.D., Srinivasan S., Fletch
Cerretti D.P., Beckmann M.P.;
"Ligands for the receptor tyrosine kinases
cDNAs encoding a family of proteins.";
Oncogene 10:299-306(1995).
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P52798; O95457;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequer
15-JUN-2002 (Rel. 41, Last annotated)
Eghrin-A4 precursor (EPH-related)
                                                                                                                                                                                                          Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
                                                                                                                                                 Glycoprote
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                             Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ006352; CAA06992.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U14188; AAC50079.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A splice variant of human ephrin-A4 encodes a soluble molecule is secreted by activated human B lymphocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Logtenberg T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aasheim H.C., Munthe E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:3224; EFNA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      IPR001799; Ephrin.
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171
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                                                                                                                                                                             GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (DEPENDING ON THE ISOFORM).
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the E., Funderud S.,
              170
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       In; 1.

DI; 3:

Signal; Alternative splicing.

POTENTIAL.

EPHRIN-A4.

REMOVED IN MATURE FORM (POTENTIAL).

N-LINKED (GLCDAC. . .) (POTENTIAL).

GPI-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
annotation update)
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Fletcher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
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er F.A., Gayle R.B. III,
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RESULT 18
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand (LERK-7) (AL-1) (ZEEPHA4).

EFNA5 OR EFNA5B OR AL1 OR EPLG7 OR LERK7.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniforme Cyprinidae; Danio.
NCBI TaxID=7955;
                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commenties requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       zebrafish.";
Development 124:655-664(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFA5
EMBL; Y09669; CAA70864.1;
ZFIN; ZDB-GENE-980526-186
                                                                                                                                                                                                                                                                                                                                                    "Two Eph receptor tyrosine kinase 1 be involved in the creation of the
                                                                                                                                                                                                                                                                                                                                                                           Brennan C., Monschau B., I
Bonhoeffer F., Holder N.;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97195707; PubMed=9043080; Brennan C., Monschau B., Lindberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                        TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
DEVELOPMENTAL STAGE: EXCRESSED IN THE PRESUMPTIVE MIDERAIN OF
DEVELOPING EMBRYOS FROM THE SIZON STAGE. BY 24 HOURS IT IS
STRONGLY EXPRESSED IN THE MIDERAIN CAUDAL TO THE PRESUMPTIVE
TECTUM, AT LATER STAGES IT IS MAINTAINED AT THE POSTERIOR MARGIN
OF THE TECTUM.
                                                                                                                                                                                                                                                                          FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLV
OF THE RETINO-TECTAL MAP.
SUBCELLULAR LOCATION: Attached to the membrane
                                                                                                                                                            SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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                                                                                                                                                                                                                                                                 (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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Pred. No. 0.0
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the
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                                                                                                                     a collaboration -
                                                                                                                                                                                                                                                                                                             CREATION
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Best Local Similarity
Matches 72; Conser
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SEQUENCE
                                                                                                                                                                                                                                                                                                                (IERK-1) (XELF).

(EFNAI OR EPGLI OR ELF.

Xenopus laevis (African clawed frog).

Xenopus, Metazoa, Chordata, Craniata, Vertebrata, E

Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea,

Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                           P52734,
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                            MEDLINE=97000306; PubMed=8843391; Weinstein D.C., Rahman S.M., Ruiz J.C., Hemm "Embryonic expression of eph signalling fact Mech. Dev. 57:133-144(1996).

Mech. Dev. 57:133-144(1996).

EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Developmental
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          CBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 LLLLGVLGLVSGLSLEP-------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA 65
                                                                                                                                         similarity).
SIMILARITY: BELONGS TO
                                                                                                                                                                   SIMILARITY).
SUBCELLULAR LOCATION: Attached to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XENLA
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U31204;
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37
228 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal
1 20 POTENTIAL.
21 228 EPHRIN-A5.
37 N-LINKED (GLCNAC. . .) (POTENTIAL).
AAA74485.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                         THE EPHRIN FAMILY.
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N-LINKED (GLCNAC. . .) (P
74B3406C05418E6E CRC64;
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Pred. No. 0.0
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LOW AFFINITY TO
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; Pipidae;
                                                                                                                                                                   a GPI-anchor
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ГО ЕРНА1
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CARBOHYD
                                                                                           MEDLINE=97392664; PubMed=9245480;
Kozlosky C.J., Vandenbos T., Park L.S., Cerretti D.P., Carpenter M.K.;
"LERK-7: a ligand of the Eph-related kinases is developmentally
regulated in the brain.";
Cytokine 9:540-549(1997).
                                                                                                                                                                                                                                                       Winslow J.W., Moran P., Valverde J., Shih A., Tsai S.P., Goddard A., Henzel W.J., Hefti F.; "Cloning of AL-1, a ligand for an Eph-related receptor involved in axon bundle formation.", Neuron 14:973-981(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine
MEDLINE=20069483; PubMed=10601038;
Davy A., Gale N.W., Murray E.W., Klinghoffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFNAS OR EPLG7
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ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
Glycoprotein; GPI-anchor;
                                                     FUNCTION
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                 TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95267434; PubMed=7748564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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Primates;
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1.
Alternative splicing;
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N-LINKED (GLCNAC. . .) (POTENTIAL).

TPPPVNVHTPRSHIQSDEPEVPLPGVMKSVAGNSAAPGTPC

TLYGLLLAALLIRL -> SE (IN ISOFORM A').

1B3A508E0A7B872E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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     Soriano
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RESULT 21
EFA5_MOUSE
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Best Local S
Matches 65
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VARIANT
                       EPRAS MOUSE STANDARD; PRT; 228 AA.

008543; 008544;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine
(LERK-7) (AL-1).
EFNAS OR EPLG7 OR LERK7 OR EPL7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feuerstein C., Robbins S.M.; "Compartmentalized signaling by GPI-anchored ephrin-A5 requires the Fyn tyrosine kinase to regulate cellular adhesion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN; 1.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U26403; AAB60377.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: BINDS TO THE RECEPTOR TYROSINE EPHBI.
SUBCELLULAR LOCATION: ATTACHED TO THE ME IS COMPARTMENTALIZED IN DISCRETE CAVEOLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE DEV. 13:3125-3135(1999).

FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.

INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAB-LIKE

MEMBRANE MICRODOWAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF I

COGNATE RECEPTOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF

THE FYN TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHTSKGFKRWECNRPHSPN------GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PADDTV---HESAEPSRG-ENAAQTPRIPSRL----LAILLFLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI PDNGRRS
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37
55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE
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EPHRIN-A5.

N-LINKED (GLCNAC. . .) (PORTING PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PROPERTIES OF PR
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Pred. No. 0.001
29; Mismatches
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                                                                                                            kinase
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RESULT 22
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AC P97605;
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-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND EPHB1 (BY SIMILARITY).

-!- SUBCELULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT IS COMPARIMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
MICRODOMAINS (BY SIMILARITY).

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Publiken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
"Distinct and overlapping expression patterns of ligands for Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1996).
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VARSPLIC
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U90664; AAB50239.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Developmental
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                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:107444; Efna5.
rPro; IPR001799; Ephrin.
                                                                                                                                                                              S---DGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
                                                                                                                                                                                                                                                                      VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC
                                                                                                                                                                                                                                                                                                 VYWNSANKRFOAEGGYVLYPOIGDRIDLICPRARPGGHSSPNYEFYKLYLVG-----
                                                                                                                    PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA 243
                                                                                                                                                                                                            DHTSKGFKRWECNRPHSPN------GPLKFSEKFOLFTPFSLGFEFRPGREYFYISS
                                                                                        PADDTV---HESAEPSRG-ENAAQTPRIPSRL----LAILLFLLA
                                                                                                                                                   AIPDNGRRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00812; Ephrin;
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                         -GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
                                                                                                                                                                                                                                                                                                                                                                                           228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    splicing.
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; Neurogenesis; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                              9.1%;
                                                                                                                                                                                                                                                                                                                                                                                            26339
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                                                                                                                                                   CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE
                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                Score 167.5;
Pred. No. 0.00
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.

EPHRIN-A5.

N-LINKED (GLCNAC. . .) (PO
MISSING (IN SHORT ISOFORM)
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                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signal;
                                                                                                                                                                                                                                                                                                                                   Gaps
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Best Local S
Matches 65
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Li Y.Y., McTiernan C.F., Feldman A.M.;

Li Y.Y., McTiernan C.F., Feldman A.M.;

rierk7, rat ligand for Eph-related receptor tyrosine kinase.";

Submitted (MAR-1998) to the EMEL/GenBank/DDBJ databases.

Submitted (MAR-1998) to the EMEL/GenBank/DDBJ databases.

-I-FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.

-INDUCES COMPARIMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELULAR DOMAIN OF ITS MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELULAR DOMAIN OF ITS
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=Sprague-Dawley;
MEDLINE=95267434; PubMed=7748564;
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
Ephrin-A5 precursor (EPH-related receptor t
(LERK-7) (AL-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U69279; AAC05801.1; -. InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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142
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SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE MICRODOWALNS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, PLACENTA AND LUISING SPECIFICITY: EXPRESSED IN BRAIN, HEART, PLACENTA AND LUISINILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF THE FYN TYROSINE KINASE (BY SIMILARITY).
SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
                                                S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
                                                                                                DHTSKGFKRWECNRPHSPN------GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS
                                                                                                                                                                                                    VYWNSSNPRFO-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC
                                                                                                                                                                                                                                                  VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYBFYKLYLVG------
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                                                                                                                                                                                                                                                                                                     h 9.1%;
Similarity 28.8%;
65; Conservative 29
                                                                                                                                                    GAQGRRCEAPPAPALLLTCDRPDLDLRFTIKFQEYSPALWGHEFRSHHDYYIIAT
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37
228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.

1 20 POTENTIAL.
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37
26358
  -CLK--LKVFVR----PTNSCMKTIGVRDRVFDVNDKVENSLE
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                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                  Score 167.5;
Pred. No. 0.00
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           EPHRIN-A5.
N-LINKED (GLCNAC. . .) (F
, 855985532D580022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                        .00019;
es 81;
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, Beck K.D., Caras
i tyrosine kinase
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                                                                                                                                                                                                                                                                                                                                                           228;
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18 LIGVIGIVSGISIEPYYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPN--

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  Matches
                        Query Match
                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                EFAL HUMAN STANDARD; PRT; 205 AA.

P20827;

01-FEB-1991 (Rel. 17, Created)

01-FEB-1991 (Rel. 17, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)

(LERK-1) (Immediate early response protein B61) (Tumor necrosis factor, alpha-induced protein 4).

EFNA1 OR EPGL1 OR LERK1 OR TNFAIP4.

Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 23
HUMAN
                                                                                                       Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
PRODOM; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91042512; PubMed=2233719;
Holzman L.B., Marks R.M., Dixit V.M.;
Holzman i.B., Marks R.M., Dixit V.M.;
"A movel immediate-early response gene of endothelium
cytokines and encodes a secreted protein.";
Mol. Cell. Biol. 10:5830-5838(1990).
                                                                                CHAIN
                                                                                            Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPI-ANCHOK.
MEDLINE=95140419; PubMed=7838529;
Maraskovsky E., McGrew J.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Euthería;
                                                                                                                                                                                                                   PIR; A36377; A36377
                                                                                                                                                                                                                              EMBL; M57730; AAA58388.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                         MIM; 191164;
                                                                                                                                                                            InterPro; IPR001799; Ephrin.
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              Local
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46;
                                                                                                                                                                                                      HGNC:3221; EFNA1.
               Similarity
                                                   1
18
26
205 AA;
 Conservative
                                                   205 E
26 N
23771 MW;
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Primates;
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              9.0%;
27.5%;
 31;
                                                                POTENTIAL.
EPHRIN-A1.
N-LINKED (G
Score 166; DB
Pred. No. 0.00
%1; Mismatches
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                                                      4FEFC6BF4C1251A9
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                                                        CRC64;
                         Length
  Indels
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  16;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)
(LERK-1) (Immediate early response protein B61).
EFNAL OR EFGLI OR LERKI.
EFNAL OR EFGLI OR LERKI.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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P97553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takahashi H., Ikeda T.;
"Molecular cloning and expression of rat and implications on organogenesis.";
Oncogene 11:879-883(1995).
-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KEPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH I
                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
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MEDLINE=95405853; PubMed=7675446;
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PRODOM; PD002533; EPHRIN, 1.
PROSITE, PS01299, EPHRIN, 1.
Glycoprotein; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
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YYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERD-----
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                                           RYSLYMVEHQEYVTCEPQSKDQVRVKCNQPSAKHGPEKLSEKFQRFTPFTLGKEFKEGHS 125
                                                                                                                               LLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG
                                                                      FYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHD 134
                                                                                                    LLGLCCSLAAVDRHIVFWNSSNPKFREE-DYTVHVQLNDYLDIICPHYEDDSV-ADAAME
                                                                                                                                                                                                                                                                                                                                                                                             s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                     205 AA;
                                                                                                                                                            Conservative
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26
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23718 MW;
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                                                                                                                                                                                                                  POTENTIAL.

EPHRIN-A1.

N-LINKED (GLCNAC. . .) (P., CB6DAB3DB56A6EAD CRC64;
                                                                                                                                                                         Score 162.5; DB 1
Pred. No. 0.00036;
                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   It is produced through
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                                                                                                                                                                                       DB 1;
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O EPHA1
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            CHAIN
CARBOHYD
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
"Distinct and overlapping expression patterns of ligands for Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1996).

-I- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4, EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takahashi H., Ikeda T., molecular cloning and expression implications on organogenesis.", Oncogene 11:879-883(1995).
                                                                                                        EMBL; D38146; BAA07344.1; -.
EMBL; U26188; AAA67563.1; -.
EMBL; U90662; AAB50237.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morris J.C., Ciarletta A., Morris G.E., Giannotti Hammett D.J., Finnerty H., Turner K., Wood C.R.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFNAI OR EPGLI OR LERKI OR EPL1.
Mus musculus (Mouse).
   CONFLICT
                                                                                  Glycoprotein;
SIGNAL
                                                                                                                                                                    MGD; MGI:103236; Efnal.
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                      - ! - SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97060319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                          Pfam; PF00812; Ephrin; 1
PRINTS; PR01347; EPHRIN.
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                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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   118
126
174
181
191
                                                                                                   GPI-anchor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8903354;
                                                                                                1.
Signal
POTENTIAL.
EPHRIN-A1.
N-LINKED (GLCNAC. .
H -> Y (IN REF. 1).
A -> T (IN REF. 1).
Q -> E (IN REF. 1).
N -> K (IN REF. 1).
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Matches 43
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                                                         This SWISS-PROT entry is copyright. It is produced through a collail between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contenting remitters.
                                                                                                                                                                                                                                                                                                                                                                                                                 008542; 055218;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                  "Characterization of the genes for mouse LERK-3/Ephrin-A3 mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 conservation of intron/exon structure."; Genomics 47:131-135(1998).
 EMBL;
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                     Eph-related receptor tyrosine Dev. Biol. 179:382-401(1996). [2]
                                                                                                                                                                                                                                                                        Flenniken A.M., Gale N.W., Yancopoulos G.D., We "Distinct and overlapping expression patterns "Eph-related receptor tyrosine kinases during "
                                           or send
                                                    entities requires a license agreement
                                                                                                                                - I - SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                          Cerretti D.P.,
                                                                                                                                                                                                                      MEDLINE=98126446; PubMed=9465306;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=129;
                                                                                                                                                                                                                                                                                                          MEDLINE=97060319; PubMed=8903354;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                           similarity).
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U90663; AAB50238.1; -.
U92890; AAC39962.1; -.
U92889; AAC39962.1; JOJ
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                                           email to license@isb-sib.ch).
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Rodentia;
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Pred. No. 0
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Sciurognathi;
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                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
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Best Local
SEQUENCE OF 51-680
STRAIN=DBA/2J;
MEDLINE=92267014; F
Apte S.S., Seldin M
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SITE
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Q05306;

01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence up

01-NOV-1995 (Rel. 32, Last annotation

COLLEGE alpha 1(X) chain precursor.
                                                                                     STRAIN=129/Sv; TISSUE=Liver;
STRAIN=129/Sv; TISSUE=Liver;
MEDLINE=93238750; PubMed=8477738;
Kong R.Y.C., Kwan K.M., Lau E.T.,
Kong R.Y.C., Kwan K.S.E.;
                                                                                                                                                                        Elima K., Eerola I., Rosati R., Metsaranta M., Garorato b de Crombrugghe B., Vuorio E.,
"The mouse collagen X complete nucleotide sequence,
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
                                                      "Intron-exon structure, alternative the mouse collagen X gene, Colloa-1. Eur. J. Biochem. 213:99-111(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                          structure and expression pattern."; Biochem. J. 289:247-253(1993).
                                                                                                                                                                                                               MEDLINE=93143676; PubMed=8424763;
                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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GPI-anchor; Signal
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 PubMed=1587271;
M.F., Hayashi M
                                  FROM N.A.
                                                                                                                                                                                                                                                                      ; Chordata; ; Rodentia;
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Pred. No. 0.0
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N-LINCED (GLCNAC. . .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
MRLL -> MLLRLGLIYPPTRPPAPPGPLV (IN REF.
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EMBL; X65121; CAA46237.1; -.
EMBL; X65121; CAA46231.1; -.
EMBL; Z21610; CAA79736.1; -.
EMBL; Z2807; S2807.
PIR; S22216; S31216.
PIR; S22215; S22215.
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InterPro; IPR001087; C01lagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; C01lagen; 9.
PRINTS; PR00007; C0MPLEMNTC1Q.
PRODOM; PD000007; C01lagen; 2.
SMART; SM00110; C1q; 1.
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Biochim. Biophys. Acta 1130:78-80(1992).
-i-FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
CHAIN
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- SUBUNIT: HOMOTRIMER.

-I- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

-I- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.

-I- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92182017; PubMed=1543751;
Elima K., Metsaeranta M., Kallio J.,
Garofalo S., de Crombrugghe B., Vuor
"Specific hybridization probes for m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF
STRAIN=C57BL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular matrix; Connective tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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-GPSGVGRRGENGFPGQPGI----
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ilarity 25.5%;
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COLLAGE REGION (NC2).

TRIPLE-HELICAL REGION.

NONHELICAL REGION (NC1).

C1Q.

L (IN REF. 3).

A -> S (IN REF. 2).

L -> F (IN REF. 3).

T -> S (IN REF. 3).

T -> C (IN REF. 3).

T -> Y (IN REF. 3).

T -> Y (IN REF. 3).

T -> Y (IN REF. 3).

T -> Y (IN REF. 3).

T -> Y (IN REF. 3).

T -> Y (IN REF. 3).

T -> Y (IN REF. 3).
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Pred. No. 0.002;
0; Mismatches 108;
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FE984CA99AF708E2
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lo E.;
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Lang H., Glanville R.W., Fietzek P.P.,
"The covalent structure of calf skin tyn
acid sequence of the cyanogen bromide pe
(positions 552-788).";
Hoppe-Seyler's Z. Physiol. Chem
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Eukaryota; Metazoa; C
Mammalia; Eutheria; C
Bovidae; Bovinae; Bos
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                                                                                                                amino acid sequence of the cyanogen bromide peptide alph
(positions 403-551).";
                                                                                                                                                                                                                                                                                       "The covalent structure of calf skir acid sequence of the amino terminal (positions 1-222).", Hoppe-Seyler's Z. Physiol. Chem. 360 [2]
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20-MAR-1987 (Rel. 04, Last seq
16-OCT-2001 (Rel. 40, Last ann
Collagen alpha 1(III) chain.
                                                                                                                                            MEDLINE=80026028; PubMed=488908;
Bentz H., Fietzek P.P., Kuhn K.;
"The covalent structure of calf skin
                                                                                                                                                                                                                 MEDIINE-80026027, PubMed=488907;
Dewes H., Fietzek P.P., Kuhn K.;
"The covalent structure of calf
acid sequence of the cyanogen br
(positions 223-402).";
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-242.
MEDLINE=80026026;
                                                                                                  Hoppe-Seyler's
[4]
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MEDLINE=80026027; Pu
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bromide peptide
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                                  k P.P., Kuhn K.;
skin type III collagen.
romide peptide alpha 1(IJ
                360:841-850(1979).
                                                                                                           360:833-840(1979).
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01-AUG-1990 (Rel.
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"The covalent structure of calf skin type III collagen. VI. The amino acid sequence of the carboxyterminal cyanogen bromide peptide alpha 1(III)CB98 (positions 928-1028).";

Hoppe-Seyler's Z. Physiol. Chem. 360:861-868(1979).

-I- FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SOFT CONNECTIVE TISSUES ALONG WITH TYPE I COLLAGEN.

-I- SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS. THE CHAINS ARE LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS. TRIMERS ARE ALSO CROSS-LINKED VIA HYDROXYLYSINES.

-I- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 809-947.

MEDLINE-80028030; PubMed-488910;

Dewes H., Fietzek P.P., Kuhn K.;

"The covalent structure of calf skin type III collagen. V. The acid sequence of the cyanogen bromide peptide alpha 1(III)CB9A (position 789-927).";
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Probom; PD000007; Collagen; 1.
PROSITE; PS01208; VWFC; PARTIAL.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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MEDLINE=80026031; PubMed=488911;
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26.5%;
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HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                 Score 154.5; DB
Pred. No. 0.006;
9; Mismatches
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I; 8EEC33D1C66EC9A3 CRC64;
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                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                            Length 1049;
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                                                                                                                                                                                                                                                           Signal
SIGNAL
                                                                                                                                                                                                                                                                                             Wormbep; W0186.7; CE03759.
InterPro; IPR002486; Col cuticle_N.
InterPro; IPR002087; Collagen.
Pfam; PF01391; Collagen; 2.
Pfam; PF01484; Col_cuticle_N; 1.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; J01048; AAA27990.1; -.
EMBL; V00148; CAA23464.1; -.
EMBL; Z68301; CAA92620.1; -.
PIR; B31219; B31219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=85105075; PubMed=2578467;
Kramer J.M., Cox G.N., Hirsh D.;
"Expression of the Caenorhabditis elegans collagen genes col-2 is developmentally regulated.";
J. Biol. Chem. 260:1945-1951(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kramer J.M., Cox G.N., Hirsh D.; "Comparisons of the complete sequences Caenorhabditis elegans.";
                                                                                                                                                                                                                                                                                     Cuticle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coles L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 30:599-606(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
MEDLINE=83050944; 1
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 189
                           218
                                                      129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
FUNCTION: NEWATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXORKELETON AND AS A
BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE CUTICULAR COLLAGEN FAMILY.
 GPAGPAGNDGAPGAPGG----PGEPGASEQGGP-
                           GPLPPPSMPAVAGAAGGLALLLLGVAGA----GGAMCWRRRRAKPSESRHPGP-GSFGRGG
                                                GNPGKGASAFCEPVTQPFCQPCPGGPPGPAGPAGPAGPPGPPGPDGNPGSPAGPSGPGPAGPP
                                                                              GQSPRGGAVPRKPVSEMPMERDRG------AAHSLEPGKENLPGDPT--SNATSRGAE
                                                                                                                       Similarity
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85
105
153
183
215
301 AA;
                                                                                                        Conservative
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301
97
134
176
212
                                                                                                                                                                                                                                                                                     tissue;
                                                                                                                     8.2%;
                                                                                                                                                             28025 MW;
                                                                                                        15;
                                                                                                                                                            CUTICLE COLLAGEN 2.
GLY-RICH.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
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TRIPLE-HELICAL REGION.
                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                     Score 151.5; DB 1;
Pred. No. 0.0027;
                                                                                                          Mismatches
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 -GEPGPAGPPGPAGPAGNDG
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                                                                                                          Indels
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                                                                                                                                     301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., VARIANTS AS E-297; R-407; R-640; R-1167; Q-1215; S-1277; T-1330; E-1334; E-1347 AND C-1661, AND VARIAN E-162; Y-326; H-408; R-451; L-574; E-1269 AND P-1474.
MEDLINE=21064696; Pubmed=11134255; Heidet L., Arrondel C., Forestier L., Cohen-Solal L., Mollet Gutterrez B., Stavrou C., Gubler M.C., Antignac C.; "Structure of the human type IV collagen gene COL4A3 and mutat autosomal Alport syndrome."; J., Am. Soc. Nebhrol 12227
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[5]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCDLINE=91353570; PubMed=1882840;
MORTISON K.E., Mariyama M., Yang-Feng T.L., Reeders S.
"Sequence and localization of a partial cDNA encoding
3 chain of type IV collagen.";
2.m., J. Hum. Genet. 49:545-554(1991).
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                                                        Ding J.;
Submitted (JAN-1993)
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Mammalia; Eutheria;
       SEQUENCE
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                                                                                                                                                                                                                                                                    to be
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89:592-
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                                                                                                                                                                                                                                                                                                                                                        PubMed=1737849;
                                                                                                                                                                                                                                                                of the human Goodpasture chain of type IV collagen.
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Primates;
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-601(1992)
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VARIANTS R-43;
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1. SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALFHA 1(IV)-ALFHA 6(IV), EACH OF WHICH CAN FORM A TRIBLE HELIX STRUCTURE WITH 2 COTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.

1. SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).

1. ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THEIR 3/L5, ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THEIR C-TERMINAL NC1 DOWAINS.

1. COCHLEA, LUNG AND PRESENT ONLY IN BASEMENT MEMBRANES OF KIDNEY, EYE, COCHLEA, LUNG AND BRAIN.

1. DOWALN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE COCHLEA, LUNG AND BRAIN.

1. DOWALN: ALFHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOWALN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE GAY.Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOWAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL JOBAIN.

1. POM: PROLINES AT THE THIRD POSITION OF THE TRIPLETIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

1. PIM: THE ALTERNATIVE SPLICED FORM V CONTAINS AN ADDITIONAL N-LINKED GLYCOSYLATION SITE.

1. PIM: TYPE IV COLLAGENS CONTAIN NUMBEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF THE STATEMENT OF THE TOTOLAGENS TYPE TO COLLAGENS ON TAXIN ARE CONSERVED IN ALL KNOWN TYPE TO COLLAGENS IN THE SILULATION ARE CONSERVED IN ALL KNOWN TYPE TO COLLAGENS IN THE SILULATION ARE CONSERVED IN ALL KNOWN TYPE
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"Mutations in the type IV collagen alpha 3 (COL4A3) gene in autos "mutations in the type IV collagen alpha 3 (COL4A3) gene in autos recessive Alport syndrome.";

Hum. Mol. Genet. 3:1269-1273(1994).

-I- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT GLONERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE' MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
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Ninomiya Y.;
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MEDLINE=94124597;
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Lemmink H.H., Mochizuki T.,
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IV COLLAGENS.

IV COLLAGENS.

PTM: Phosphorylated by the Goodpasture antigen-binding protein.

PIME PROSPHORYLATED LIST THE NC1 DOWAIN OF ALPHA3(IV) MEDIATE

DISEASE: ANTIBODIES AGAINST THE NC1 DOWAIN OF ALPHA3(IV) MEDIATE

THE HUMAN AUTOLMMUNE DISEASE, GOODPASTURE SYNDROME, WHICH IS

CHARACTERIZED BY HEMATURIA AND PULMONARY HEMORRHAGE.

DISEASE: DEFECTS IN COL4A3 ARE ASSOCIATED WITH THE TYPE I

AUTOSOMAL RECESSIVE FORM OF ALFORT SYNDROME, AN HEREDITARY

GLOMERULONEPHROPATHY CHARACTERIZED BY PROGRESSIVE REMAL FAILURE,

GLOMERULONEPHROPATHY CHARACTERIZED BY PROGRESSIVE REMAL FAILURE,

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2; Mismatches 146;
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                             Proc.
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CHARACTERIZATION
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Mammalia; Eutheria;
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Rodentia;
                             U.S.A.
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    AND
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SEQUENCE FROM N.A. (SHORT AND LONG ISOFORMS).

Rehn M., Hintikka E., Pihlajaniemi T.;

"Characterization of the mouse gene for the alpha-1 chain of type
XVIII collagen (COL18A1) reveals that the three variant N-terminal
polypeptide forms are transcribed from two widely separated
promoters.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (SHORT ISOFORM).

STRAIN-BAIB/C; TISSUE-Liver;
MEDLINE-9245707; PubMed-8188673;

Rehn M.V., Hintikka E., Pihlajaniemi T.;

"Primary Structure of the alpha 1 chain of mouse type XVIII collag
partial structure of the corresponding gene, and comparison of the
alpha 1(XVIII) chain with its homologue, the alpha 1(XV) collagen
                                                                                    MEDIINE=94240111; PubMed=8183893; Ob S.P., Kamagata Y., Muragati Y., "Isolation and sequencing of cDNa; of Gly-Xaa-Yaa repeats identify a c
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 213-1140 FROM N.A. (SHORT MEDLINE=94240112; PubMed=8183894; Rehn M.V., Pihlajaniemi T.;
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annotation
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precursor (Contains:
                                            91:4229-4233(1994)
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Sciurognathi;
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Murinae; Mus
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multiple domains
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3D-structure.
SIGNAL
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                                                                                                                                                                     Pfam; PF01391; Collagen; 8.
Pfam; PF02210; TSPN; 1.
SMART; SM00282; LamG; 1.
SMART; SM00210; TSPN; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cell adhesion; Collagen; Glycoprotein; Signal; Alternative splicing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>:</del>
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A SHORT FORM AND A LONG FORM (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPFIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
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10166-1664(1998).
J. 17:1656-1664(1998).
PUNCTION: ENDOSTATIN POTENTLY INHIBITS ENDOTHELIAL CELL
PROLIFERATION AND ANGIOGENESIS. MAY INHIBIT ANGIOGENESIS
PROLIFERATION AND HEPARAN SULPHATE PROTEOGLYCANS INVOLVED IN
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rPro; IPR000087; Collagen.
rPro; IPR001791; Laminin_G.
rPro; IPR003129; TSPN.
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   TRIPLE-HELICAL REGION 1 (COL1).
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DDMEGS-GIPLWTTARSSDGLQGPPGSP
                             EKVSGDYGHPVYIVQ----DGPPQSP
                                                                                           RAKPSESRHPGP-GSFGRGGSLGLGGGGGGGGREAEFGELGIALRGG--GAADPPFCPHY
                                                                                                                                                          PGKENLPGDPTSNATSRGAEGP--LP-PPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRR
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TRIPLE-HELICAL REGION 3 (CO
NONHELICAL REGION 4 (NC4).
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Pred. No. 0.0
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MISSING (IN SHORT ISOFORM).
AVPTOLIPFOGNICAREGRESAPPDF -- MAPRWHLLDVL
TSLVLLLYARVSWAE (IN SHORT ISOFORM).
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NONHELICAL REGION 10 (NC10).

TRIPLE-HELICAL REGION 10 (COL10).

NONHELICAL REGION 11 (NC11).

N-LINKED (GLCNAC. .) (POTENTIAL

N-LINKED (GLCNAC. .) (POTENTIAL
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RESULT 32 CAFF_RIFPA ID _CAFF_RIFPA AC P30754;

STANDARD;

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TISSUE=Cartilage;
MEDILINE=91113131; PubMed=1703407;
Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.;
Thomas J.T., Kwan a.P.L., Grant M.E., Boot-Handford bovine
"Isolation of cDNAs encoding the complete sequence of bovine
"Isolation of cDNAs encoding the complete sequence of mammalian type
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VARIANT
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Blochem. J. 273:141-148(1991).
Blochem. J. 273:141-148(1991).
-i- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
-i- SUBUNIT; HOMOTRIMER.
-i- SUBUNIT; HOMOTRIMER.
-i- SUBUNIT; HOMOTRIMER.
-i- PIM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEA UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-i- SINILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
-i- SINILARITY: CONTAINS 1 CIQ DOMAIN.
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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CALH HUMAN STANDARD;
P39060; Q9Y6Q8; Q9Y6Q7; Q9UK38;
01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
COLlagen alpha 1(XVIII) chain precursor (Contains:
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Homo sapiens (Human).
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Mammalia; Eutheria; Primates;
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Pfam; PF00391; Collagen; 9.
PRINTS; PR00007; COMPLEMNTC1Q.
ProDom; PD000007; Collagen; 1.
SMART; SM00110; C1Q; 1.
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Extracellular matrix; Connective
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InterPro; IPR000087; Collagen.
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nilarity 24.2%;
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HYDROXYLATION (BY S:
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NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
C10.
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Pred. No. 0.016;
0; Mismatches 125;
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  Craniata; Vertebrata;
Catarrhini; Hominidae
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    Hominidae;
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    Euteleostomi; Homo.
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Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
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                                                                                                                                                                                                                                                               VARIANT ASN-1437.
MEDLINE=21518361;
                                                                                                                                                                                                                                                                                                                                                              Sertie A.L., Sossi V., Camargo A.A., Passos-Bueno M.R.;
                                                                                                                                                                                                                                                                                                                                                                                         INVOLVEMENT IN KNOBLOCH SYNDROME. MEDLINE=20400145; PubMed=10942434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhi-Yong H.,
"Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 405:311-319(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Placenta;
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InterPro; IPR001791; Laminin G
InterPro; IPR003129; TSPN.
Pfam; PF01391; Collagen; 7.
Pfam; PF02210; TSPN; 1.
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EMBL; AF184060; AAF01310.1; ALT_INIT.
HSSP; P39061; INCE
GlycoSuiteDB; P39060; -.
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EMBL; AF018082; AAC39659.1; -.
EMBL; AL163302; CAB90482.1; -.
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SMART; SM00210; TSPN; 1.
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FTIG=CAR OOO150.

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GY SIMILARITY.

CELL ATTACHMENT SITE (POTENTIAL).

MISSING (IN SHORT ISOFORM).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
      SEQUENCE FROM N.A.
MEDLINE-92250566; PubMed=1577778;
Har-El R., Sharma Y.D., Aguilera A., U
Eyre D.R., Juricic L., Chandrasekaran
Upholt W.B., Tanzer M.L.;
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PIR; S22918; S22918.
InterPro; IPRO00087; Collagen.
Pfam; PF01391; Collagen; 1.
ProDom; PD000007; Collagen; 1.
Excracellular matrix; Connective tis
Glycoprotein; Cartilage; Collagen; S
          Homo sapiens (Human).
Eukaryota, Metazoa, C
Mammalia, Eutheria; P
NCBI_TaxID=9606;
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Primates;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                              -CA19 HUMAN STANDARD; PRT; 921 AA. P20849; Q9Y6P2; Q9Y6P3; Q9H151; Q9H152; Q9922 01-FEB-1991 (Rel. 17, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Collagen alpha 1(IX) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVGOSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSM
                                                                                                                                                                                                                                                                                                               PGPPGPPGMPGFKGHTGHKGGPGBIGKEGEKGSPGPPGPPGI
                                                                                                                                                                                                                                                                                                                                                          -GAADPPFCPHYEKVSGDYGHPVYIVQDGP-----PQSPPNI
                                                                                                                                                                                                                                                                                                                                                                                                       PGPPGPPGPSGLPGGNGFRGPPGPSGLPGFPGPPGPPGLAGIIPEGGGDLQCPALCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGAAGEAGLPGLP----GVDGLTGT-----DGPPGPNGPPGDRGALGPAGPPGPAGKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAVAGAAG--GLALLLLGVAGAGGAMCWRRRRAKPSESRHPG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVG--PQGPPGPRGPPGPSGKDGIDG----EPGPSGLPGPP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GSLGLGGGGGM----GPR-----EAEPGELGIALRGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLAGEN ALPHA 3 (IX) CHAIN.
TRIPLE-HELICAL REGION 3 (COL3).
NONHELICAL REGION 2 (COL2).
TRIPLE-HELICAL REGION 2 (COL2).
NONHELICAL REGION 1 (COL).
TRIPLE-HELICAL REGION 1 (COL).
TRIPLE-HELICAL REGION 1 (COL).
NONHELICAL REGION 1 (NC1).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GICNAC. . .) (POTENTIAL)
N-LINKED (GICNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 144; DB Pred. No. 0.01 9; Mismatches
Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                            RT; 921 AA.
Q9H152; Q99225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue; Repeat; Hydroxylation;
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                                                                                                                                                                                                                                                                                                                                                            336
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                       Euteleostomi;
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                                                                                                                                                                            Q13700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GPKGAPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muragaki Y., Nishimura I., Henney A., Ninomiya Y., Olsen B.R.; "The alpha 1 (IX) collagen gene gives rise to two different transcripts in both mouse embryonic and human fetal RNA."; Proc. Natl. Acad. Sci. U.S.A. 87:2400-2404(1990).
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Nickerson T., Harley J.;
Submitted (DEC-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human COL9A1 and COL9A2 genes. Two genes of 90 and 15 kb code for similar polypeptides of the same collagen molecule."; Matrix Biol. 17:237-241(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olsen B.
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MEDLINE-89137096; PubMed-2465149;
Kimura T., Mattei M.-G., Stevens J.W., Goldring M.B., Ninomiya Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of rat and human type IX collagen cDNA and localization of the alpha 1(IX) gene on the human chromosome (Eur. J. Biochem. 179:71-78(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING, DOMAIN: EACH SUBURIT IS COMPOSED OF THREE TRIPLE-RELICAL DOMAINS INTERSPERSED WITH NONCOLLAGENOUS DOMAINS. THE GLOBULAR DOMAIN AT THE WITH NONCOLLAGENOUS DOMAINS. THE GLOBULAR DOMAIN AT THE WITH POLYANION OF TYPE IX COLLAGEN WOLECULES REPRESENTS THE NC4 DOMAIN WHICH MAY PARTICIPATE IN ELECTROSTATIC INTERACTIONS WITH POLYANIONIC GLYCOSAMINGUYCANS IN CARTILLAGE.

PTM: COVALENTLY linked to the telopeptides of type II collagen by the covalently linked to the telopeptides of type II collagen by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the ey SUBUNIT: 3 (IX) cha
L; X54412; CAA38276.1; -.

L; X54413; CAA38277.1; -.

L; AF03613; AAC33527.1; JOINED.

L; AF036110; AAC33527.1; JOINED.

L; AF036111; AAC33527.1; JOINED.

L; AF036112; AAC33527.1; JOINED.

L; AF036114; AAC33527.1; JOINED.

L; AF036114; AAC33527.1; JOINED.

L; AF036115; AAC33527.1; JOINED.

L; AF036116; AAC33527.1; JOINED.

L; AF036117; AAC33527.1; JOINED.

L; AF036118; AAC33527.1; JOINED.

L; AF036119; AAC33527.1; JOINED.

L; AF036119; AAC33527.1; JOINED.

L; AF036119; AAC33527.1; JOINED.

L; AF036119; AAC33527.1; JOINED.

L; AF036119; AAC33527.1; JOINED.

L; AF036119; AAC33527.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lysine-derived cross-links.

PIM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 okko L.;
1 COL9A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heterotrimer of a alpha 1(IX), a alpha 2(IX) and a
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MBL outstation -
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EMBL; ALL.

R EMBL; M32137; AAA.53474...

R EMBL; M32133; AAA53475.1; -.

DR EMBL; M32135; AAA53475.1; JOINED.

PIR; S02140; S02140.

PR; S13580; S13580.

PR; S13580; S13580.

Genew; HGNC:2217; COL9A1.

Genew; GANGE: COL9A1.

Genew; GANGE: COL9A1.

Genew; GANGE: COL9A1.

Genew; GANGE: COL9A1.
DOMAIN
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VARSPLIC
VARSPLIC
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Pfam; PF02210; TSPN; 1.
ProDom; PF0000007; Collagen; 1.
SMART; SM00210; TSPN; 1.
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                         CONFLICT
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InterPro; IPR001791; Laminin_C
InterPro; IPR003129; TSPN.
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AF036122;
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MW.
                       N-LINKED (GLCNAC, ...) (POTENTIAL).
MISSING (IN SHORT ISOFORM).
PLEPRETCHELPARITPSQTTDE -> MAWTARDRGALGI
LLLGLCLCAAQ (IN SHORT ISOFORM).
PP -> AS (IN REF. 1).
I -> L (IN REF. 1).
Q -> R (IN REF. 2).
AGGRAENKGPDP -> LVSEHLTKGLTLERLTAAWLSA
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NONHELICAL REGION (NC4).
TRIPLE-HELICAL REGION (C3).
TRIPLE-HELICAL REGION (C3).
TRIPLE-HELICAL REGION (NC2).
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BY SIMILARITY.
BY SIMILARITY.
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 5A6822658FC44B34 CRC64;
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EMBL outstation

a collaboration MBL outstation -

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Matches 84
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POBLZ5;
POBLZ5;
O1-ANG-1988 (Rel. 08, Created)
O1-NOV-1991 (Rel. 20, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation updat
Collagen alpha 1(X) chain precursor.
                                                                                                                                                                                                                           open read
J. Biol.
             REVISIONS TO C-TERMINUS.

MEDLINE=89380199; PubMed=2476437;

Yamaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;

Yamaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;

"The cloning and sequencing of alpha 1(VIII) collagen cDNAs demonstrate that type VIII collagen is a short chain collagen and contains triple-helical and carboxyl-terminal non-triple-helical domains similar to those of type X collagen.";

J. Biol. Chem. 264:16022-16029(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA1A
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
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                                                                                                                         MEDIINE-89054019; PubMed=2461368;
Luvalle P., Kinomiya Y., Rosenblum N.D., Olsen B.R.;
"The type X collagen gene. Intron sequences split the 5'-untranslated region and separate the coding regions for the non-collagenous aminoterminal and triple-helical domains.";
J., Biol. Chem. 263:18378-18385(1988).
                                                                                                                                                                                     SEQUENCE OF 1-75 FROM N.A. MEDLINE=89054019; PubMed=2
                                                                                                                                                                                                                                                               Olsen
                                                                                                                                                                                                                                                                         Ninomiya Y., Gordon
                                                                                                                                                                                                                                                                                      SEQUENCE OF 48-674 FROM N.A., AND SEQUENCE MEDLINE=86168227; PubMed=3082876;
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                                                                                                                                                                                                                                                                                                                      _TaxID=9031;
                                                                                                                                                                                                                          developmentally regulated type X reading frame without introns."; iol. Chem. 261:5041-5050(1986).
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-JAN-1990
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Pfam; PF01391; Collagen; 8.
PRINTS; PR00007; COMPLEMNTC1Q.
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EMBL; J04194; AAA48634.1; -.
PIR; A31896; A31896.
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Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                            PPGPHSSPNYEFY-KLYLVG------
                                                                                                                                                                            LGLGGGGGMGPREAEPGELGI----ALRG-GGAADPPFCPHYEK---VSGDYGH--PVYIV
                                                                                                                                                                                                                                                                           RGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNAT----
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                                                                                                     -EGPPGFP
                                                                                                                                                       VGIGKPGPMGP
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                                                                                                                                                                                                                            PLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKP---
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SM00110; C1Q; 1.
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                   Created)
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     sequence
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Pred. No. 0
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TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
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NONHELICAL REGION ()
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1; 91;

674;

Indels 122;

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16;

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CRC64; Length

CHAIN

-SESRHPGP-GSFGRGGS

274

325

SRGAEG

218

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171

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15-JUN-2002 (Re Collagen alpha COL5A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87146331; PubMed=3029669; Weil D., Bernard M.P., Gargano S., Ra "The pro alpha 2(V) collagen gene is major fibrillar-forming collagens."; Nucleic Acids Res. 15:181-198(1987).
                                                                                                                                                                          VARIANT EDS-II ARG-960.
PubMed=9783710;
Richards A.J., Martin S.,
Burrows N.P.;
                                                                                                                                                                                                                                                                                 Michalickova K., Susic M., Willing M.C., Wer
"Mutations of the alpha2(V) chain of type V
assembly and produce Ehlers-Danlos syndrome
hum. Mol. Genet. 7:249-255(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94237164; PubMed-8181482;
Moradi-Ameli M.; Rousseau J.C., Kleman J.P., Champliaud M.F.,
Boutillon M.M., Bernillon J., Wallach J.M., van der Rest M.;
"Diversity in the processing events at the N-terminus of type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 264:2735-2738(1
[2]
SEQUENCE OF 398-1496 FROM N.A.
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MEDLINE=89123368; PubMed=2914927;

Woodbury D., Benson-Chanda V., Ramirez F.;

Woodbury D., Benson-Chanda V., Ramirez F.;

"Amino-terminal propeptide of human pro-alpha 2(V) collagen conforms

to the structural criteria of a fibrillar procollagen molecule.";

J., Biol. Chem. 264:2735-2738(1989).
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Eukaryota; Metazoa;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation of the alpha 3-chain of human type characterization by partial sequencing."; fiol Chem. Hoppe-Seyler 373:69-75(1992).
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MEDLINE=92239022; PubMed=1571108;
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Tsipouras P., Schwartz R.C., Liddell
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                                                                                                         Med. Genet.
                                                                                                                                                     single base mutation
                     FUNCTION: TYPE V COLLAGEN IS A MEMBER OF GROUP I COLLAGEN (FIBRILIAR FORMING COLLAGEN). IT IS A MINOR CONNECTIVE TISSUE COMPONENT OF MEARLY UBIQUITOUS DISTRIBUTION. TYPE V COLLAGEN BINDS TO DNA, HEPARAN SULFATE, THROMBOSPONDIN, HEPARIN, AND INSULIN.
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ha 2(V) chain p
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TWO ALPHA 1 (V)
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e V collagen imposme type I.";
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GPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP--

169 500

QSPRG--= ||| RGPRGDI

PGTLGPPGPVGERGAPGNRGF----

PGSDGLPGPKGAQGERGPVGSSGPKGSQ

GSFGRGG

554 273 ----DPTSNATSRGAE

217

GAV-PRKPVSEMPMERDRGAAHSLEPGKENLPG----

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Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                                                        Pfam; PF01391; Collagen; 18.
Pfam; PF01410; COLFI; 1.
ProDom; PD000007; Collagen; 5.
ProDom; PD002078; Fib_collagen_C
SMART; SM00038; COLFI; 1.
SMART; SM000214; VMC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J04478; AAA51859.1; --
EMBL; X04758; CAA28454.1; --
EMBL; M1718; AAA52058.1; --
PIR; A25374; A25374.
PIR; A25874; A25874.
PIR; A3017; A30017.
PIR; A31427; A31427.
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                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del>
                                                                                                                                                                                                                                                      Extracellular matrix; Connective Glycoprotein; Collagen; Signal; E
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000087;
InterPro; IPR000885;
InterPro; IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew;
                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                PROSITE; PS01208; VWFC; 1.
                                                                                                                                                                                                                                             isease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOST TISSUES AND TRIMERS OF ONE ALPHA 1(V), ONE ALPHA 2(V), AND ONE ALPHA 3(V) CHAIMS IN PLACENTA.

PM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

DIERASE: Defects in COL5A2 are a cause of Ehlers-Danlos syndrome gravis or type I (EDS-I), and Ehlers-Danlos syndrome mitis or type II (EDS-I), and Ehlers-Danlos syndrome is a genetically and phenotypically heterogeneous connective-tissue disorder characterized by loose-jointedness and fragile, velvety, stretchable, bruisable skin that heals with peculiar 'cigarette-paper' scars. EDS-I and EDS-II are autosomal dominant traits.

SIMILARITY: CONTAINS 1 VWFC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:2210; COL5A2
            Similarity
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293
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608
614
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1418
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614
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; VWF_C.
           7.7%;
                                              144720
                                                       HYDROXYLATION.

(FITIDE VAR 013588,

A -> P (IN REF. 6).

K -> T (IN REF. 3).

F -> Q (IN REF. 4).

V -> A (IN REF. 4).
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                                                                                                                                                    HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
Score 142.5; DB Pred. No. 0.051; Mismatches
                                                                                                                                                                                                          CARBOXYL-TERMINAL
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[
                                                                                                                                                                                                                                                       tissue; Repeat; Hydroxylation;
Ehlers-Danlos syndrome;
                                              82827C17A8644F5A
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(V)
 76;
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                       Length
                                              CRC64;
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                        1496;
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P27658; Q95D07;
01-AUG-1992 (Rel. 23, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(VIII) chain precursor (Endot
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 8.
PRINTS; PR000007; COMPLEMNTC1Q.
ProDom; PD000007; Collagen; 1.
SMART; SM00110; ClQ; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Cell adhesion; Collagen; Signal.
SIGNAL 1 28
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                                                                                                                                                                                                                      EMBL; X57527; CAA40748.1; -
EMBL; BC013581; AAH13581.1;
PIR; S15435; S15435.
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                                                                                                                                                     InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        INDITED OF THE EMBI/GENBANK/DDBJ databases.

FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEM FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEM MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.

SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIAT WITH ALPHA 2 (VIII) TYPE COLLAGENS.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEAUNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

MISCELLANGOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PROMISECULAR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PROMISECULAR STABILITY OF THIS REGION.

THE HIGH THERMAL STABILITY OF THIS REGION.

SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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                                                                                                                                                                                                       HGNC:2215; COL8A1.
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(VIII) chain
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Best Local S
Matches 72
                       SEQUENCE OF 266-1029 FROM N.A. MEDLINE-93143659; PubMed=8380980; Ibrahimi A., Bertrand B., Bardon S. Ailhaud G., Dani C.; chain of type V "Cloning of alpha 2 chain of type V mouse development."; Biochem. J. 289:141-147(1993).
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DOMAIN
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DOMAIN
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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SEQUENCE OF 266-600
STRAIN=C57BL/6; TISS
                                                                                                      SEQUENCE FROM N.A.
Ibrahimi A., Bardo
                                                                                              Submitted
                                                                                                                                                          Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                   44SQ4---
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PPGPHGLPG-----IGKPGGPGLPGQPGPK-----
                                                                                                                                                                                                                                                                                                                                                                                                          -----LRGPKGDKGFGMPGAPGVKGP-
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572 744
602 262
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4 382
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73364 MW;
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TISSUE=Fibroblast;
                                                                                             , to
                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
         FROM N.A.
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NONHELICAL REGION (NC2)
TRIPLE-HELICAL REGION
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SEQUENCE OF 659-1029 FROM N.A.

***X MEDILNE=93256888; PubMed=8489506; 
A Zhang R.Z., Pan T.C., Timpl R., Chu M.-L.; 
A Zhang R.Z., Pan T.C., Timpl R., Chu M.-L.; 
A Zhang R.Z., Pan T.C., Timpl R., Chu M.-L.; 
T "Cloning and sequence analysis of cDNAs encoding the alpha 1, alpha 1 
"Cloning and sequence analysis of cDNAs encoding the alpha 1, alpha 1 
"Cloning and sequence analysis of cDNAs encoding the alpha 1, alpha 1 
"Cloning and sequence analysis of cDNAs encoding the alpha 1, alpha 1 
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EMBL; X63322; CAA44206.1; -.
EMBL; Z18272; CAA79153.1; -.
EMBL; 106343; AAA37441.1; -.
PIR; S13745; S13745.
MGD; MG1188460; CO1562.
InterPro; IPR000087; CO11agen.
InterPro; IPR002035; VWF—A.
PERM: PRO0092; VWF—A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure of cDNAs encoding the triple-helical domain of murine alpha 2 (VI) collagen chain and comparison to human and chick homologues. Use of polymerase chain reaction and partially degenerate oligonucleotide for generation of novel cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00092; vwa; 3.
Pfam; PF01391; Collagen; 4.
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I -> S (IN REF. 3)
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ONDSL -> TGNDS (IN REF. 4)
GNDSL -> TGNDS (IN REF. 4)
                                                                                                                                                                                                                                                                                     NONHELICAL REGION.
TRIPLE-HELICAL REGION.
NONHELICAL REGION.
VWEA 1.
VWEA 2.
VWEA 3.
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Best Local
                                                                                           INTERNATIVE PRODUCTS: 2 ISOFORMS; I (SHOWN HERE) AND BETWEEN NC1

-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; I (SHOWN HERE) AND II; ARE
PRODUCED BY ALTERNATIVE SPLICING.

-I- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
DOMAIN (NC1) AT THEIR C-TERNINUS, PREQUENT INTERRUPTIONS OF THE
G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
TRIPLE-HELICAL 75 DOMAIN.

-I- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPPETIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

-I- PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF
THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
IV COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Collagen alpha 2(IV) chain precursor.
Ascaris suum (Pig roundworm) (Ascaris lumbricoides)
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridio
                                                                                                                                                                                                                                                                                                                                                                                            Pettitt J., Kingston I.B.;
"The complete primary structure of a nematode alpha 2(IV) and the partial structural organization of its gene.";
J. Biol. Chem. 266:16149-16156(1991).
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P27393;
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                                                                                                                                                                                                                                                                                                                              FUNCTION: COLLAGEN TYPE IV IS SPECIFIC FOR BASEMENT MEMBRANES SUBUNIT: TRIMERS OF TWO ALPHA 1(IV) AND ONE ALPHA 2(IV) CHAIN TYPE IV COLLAGEN FORMS A MESH-LIKE NETWORK LINKED THROUGH INTERMOLECULAR INTERACTIONS BETWEEN 78 DOMAINS AND BETWEEN NC:
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Pred. No. 0.
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RESULT 42
CA13_HUMAN S'
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DT 01-UAN-1990 (Re1
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Hydroxylation; Connective tissue;
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InterPro; IPR000087; Collagen.
InterPro; IPR001442; ProcollagnC4.
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97; Conserv
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an email to license@isb-sib.ch).
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OR 1634 (BY SIMILARITY).
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GDIGPAGPPGPPGPREFTGSGSIVGPRGHSGDKGVK
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procollagen.";
Nucleic Acids Res. 1
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MEDLINE=81208139;
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Covalent structure of collagen: amino acid sequence of five
consecutive CNBr peptides from type III collagen of human li-
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MEDLINE=77134724; FubMed=557335;
Seyer J.M., Kang A.H.;
"Covalent structure of collagen:
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MEDLINE=89350838; PubMed=2764886;
MEDLINE=89350838; PubMed=2764886;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                          Mankoo B.S., Dalgleish R.;
"Human pro alpha 1(III) collagen: cDNA
Nucleic Acids Res. 16:2337-2337(1988).
                                                                                                                                                                                                                          SEQUENCE OF 950-1466 FROM N.A. MEDLINE=88189827; PubMed=3357782;
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Earley J.J., Zhuang J., Noerrgaard O., Darling R.C., Abbott W.M.,
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infrequent cause of aortic aneurysms.";
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procollagen gene (CCL3A1).";

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MEDLINE=86187804; PubMed=3754462;
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with the type I collagen genes during fibroblast growth.";
with the type ISOllagen genes during fibroblast growth.";
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MEDITINE=85157600; PubMed=2579949;
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with aortic aneurysms.";
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VARIANT AORTIC ANEURYSM ARG-303,
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PubMed=9101290;
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TISSUE=Placenta;
MEDLINE=88303360; PubMed=3405773;
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MEDLINE=91056145; PubMed=2243125;
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of human prepro alpha (III) collagen.",
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ocollagen (COL3A1) in a family
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VARIANT EDS-IV VAL-1077.
MEDLINE=91374480; PubMed=1895316;
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MEDLINE=93022543; PubMed=1357232;
Johnson P.H., Richards A.J., Pope
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MEDLINE-92316511; PubMed=1352273;
Richards A.J., Ward P.N., Narcisi P., Nicholls A.C.,
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"The cloning and sequencing of alpha 1(VII) collagen cDNAs

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"The cloning and sequencing of alpha 1(VIII) collagen and

"The cloning and sequencing of alpha 1(VIII) collagen and

"The cloning and sequencing is a short chain collagen and

"The contains triple-helical and carboxyl-terminal non-triple-helical

"The contains similar to those of type X collagen.";

"The contains similar to those of type X collagen.";

"The contains triple-helical and carboxyl-terminal non-triple-helical

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Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Glycoprotein; Cell adhesion; Collagen; Signal.
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Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Eukaryota; Metazoa; Lagomorpha; Leporidae; Oryctolagus.
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P14282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a or send an email to
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01-NOV-1995 (Rel. 32, Last annotation update)
Collagen alpha 1(VIII) chain precursor (Endothelial collagen).
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 8.
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                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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               169
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                                                                                                                                                PPGPHSSPNYEFYKLYLVG------GAQG-RRCEAPPAPNLLLTCDRPDLDLRFT 114
                                                                  IKFQEYSPNLWGHEFRSHHDYYIIATSDGTR----EGLESLQG--
                                                                                                                                                                                                                                                                                                                                                                                                ; PR00007; COMPLEMNTC1Q,
SM00110; C1Q; 1.
E; PS01113; C1Q; 1.
                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s requires a license agreement (See http://www.isl
an email to license@isb-sib.ch).
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                  744 AA;
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118
572
609
                                                                                                                                                                                 Conservative
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1117
571
744
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----SPRGGAVPRKFVSEMFMERDRGAAHSLEPGKENLFGDP--TSN
                                                                                                                                                                                               7.6%;

    IGKPGGPGLPGQPGÅKGDRGPKGPPGP

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                                                                                                                                                                                                                                                              COLLAGEN ALPHA 1(VIII) CHAIN. MONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
C10.
                                                                                                                                                                                               Score 141;
Pred. No. 0.
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                                                                                                                                                                                 Mismatches - 108;
                                                 · GEKGFGMPGLPGLKGPPGMHGPPGPVGLPGVG
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                                                                               -GVCLTRGMKVLLRVG
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RESULT
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                                                                                                                                                                                                                                                                                                     RA Kawai J., Shihagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Mateuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carminci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Scheenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Scheenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Mynobaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.

-I- SUBUNIT: WAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION WITH ALPHA 2 (VIII) TYPE COLLAGENS.
-I- TISSUE SPECIFICITY: HIGH LEVELS IN CALVARIUM, EYE & SKIN OF NEWBORN MICE, ALSO IN VARIOUS EPITHELIAL, ENDOTHELIAL AND MESENCHYMAL CELLS.
-I- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-I- SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA18 OUSE STANDARD; PRT; /43 AA. 000780; Q9D2V4; O1-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(VIII) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Alpha'l (VIII)-collagen gene transcripts encode a short-chain collagen polypeptide and are expressed by various epithelial, endothelial and mesenchymal cells in newborn mouse tissues."; Eur. J. Blochem. 207:895-902(1992).
                                                                                                                                                                                                                              Nature 409:685-690(2001
-1- FUNCTION: MAJOR COM
                                                                                                                                                                                                                                                                                              Wynshaw-Boris A.,
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PP---FCPHYEKVSGDYGH------PVYIVQDGPP-----QSPPNI 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1499564;
ta C., Inoue M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GGGGGMGPR----EAEPGELGIALRGG--GAAD
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                                                                        THE TRIPEPTIDE REPEATING
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Best Local Sim
Matches 101;
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PROSITE; PRO1113; C10; 1.

Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Cell adhesion; Collagen; Signal.

SIGNAL 28 BY SIMILARITY.

CHAIN 29 743 COLLAGEN ALPHA 1 (VIII) CHAIN.

DOMAIN 29 117 RONHBLICAL REGION (NC2).

DOMAIN 118 571 TRIPLE-HELICAL REGION (COL1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 7.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; ClQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:88463; Col8a1.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
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EMBL; X66977; CAA47387.1; JOINED.
EMBL; AX018742; BA313183.1; -.
PIR; S23779; S23779.
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AEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGP---
                         GKPGQDGIPGQPGFPGGKGEQGLPGLPGPPGLPGVGKPGFPGPKGDRGIGGVPGVLGPR-
                                                                        PPGMHGPPGPVGLPGVGKPGVTGFPGPQGPLGKPGPPGEPGPQGLIGVPGVQGPPGMPGV
                                                                                                  -PAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG----
                                                                                                                         GPPGPHGLPGIGKPGGPGLPGQPGAKG-ERGPKGPPGPPGLQGPKGEKGFGMPGLPGLKG
                                                                                                                                                 G--AAHSL----EPGKENLPGDPTSNATSRGAEGPLPPPSM-----
                                                                                                                                                                          GKPGPQGYPGIGKPGMPGKPGAMGMPGAK------GEIGPKGEIGPMGIPGPQ
                                                                                                                                                                                                   TSDGT-----REGLESLOG--GVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDR 190
                                                                                                                                                                                                                               LRGEQGPRGEPGPRGPPGP
                                                                                                                                                                                                                                                    VGGAQGRRCE----APPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIA 139
                                                                                                                                                                                                                                                                              QQVPHMPLGKDGLSMGKEMPHMQYGKEYPHLPQYMKEIPPVPRMGKEVVPKKGKEVPLAS 115
                                                                                                                                                                                                                                                                                                          ---PH-----
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C10.
G -> R (IN REF. 2).
H -> Y (IN REF. 1).
K -> KG (IN REF. 1).
P -> A (IN REF. 2).
P -> A (IN REF. 1).
D -> H (IN REF. 1).
D -> H (IN REF. 1).
T -> P (IN REF. 2).
MPS -> NPF (IN REF. 1).
F584D85BD53897F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Score 140.5; DB 1;
Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                 PGSFGRGGSLGLGG-GGGMGPRE
                                                                                                                                                                                                                                                                                                                                                                                  135;
                                                                                                                                                                                                                              -PGLPGHGMPG----
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L outstation -
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                                                                          MEDLINE=97255959; PubMed=9101290;
Kuivaniemi H., Tromp G., Prockop D.J.;
Whitations in fibrillar collagens (types I, II, III, and XI
associated collagen (type IX), and network-forming collagen
cause a spectrum of diseases of bone, cartilage, and blood
                                                                                                                                                                                                                                   SEQUENCE OF 547-655 FROM N.A.

MEDLINE=92077285; PubMed=1743401;

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Reichenberger E. Aigner T., von the expression of type

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MEDLINE=92109659; PubMed=1764025;
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Solomon B., Grant M.E., Boot-Handford
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01-NOV-1995 (Rel. 32,
01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
VARIANTS SMCD ASP-598
MEDLINE=94136476; Pubb
                                                                                                                                                                                           REVIEW ON VARIANTS.
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Beier F., Lammi
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Reichenberger E., Beier
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Mammalia; Eutheria;
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Lammi M.B.,
1 (JUN-1996) t
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                                                                9:300-315(1997).
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-598 AND PRO-614.
PubMed=8304336;
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Beier F., Luvalle
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ne EMBL/GenBank/DDBJ
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llagen (type X)
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Wallis G.A., Rasn B., Grant M.E., Boot-Handford R.P.;
Grant M.E., Boot-Handford R.P.;
"Amino acid substitutions of conserved residues in the carboxyl-terminal domain of the alpha 1(X) chain of tyroccur in two unrelated families with metaphyseal chondoccur in two unrelated families.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-96375754; PubMed=8782043;
MEDIINE-96375754; PubMed=8782043;
Mallis G.A., Rash B., Sykes B., Bonaventure J., Maroteaux P.,
Zabel B., Wynne-Davies R., Grant M.Z., Boot-Handford R.P.;
Zabel B., Wynne Davies R., Grant M.Z., Boot-Handford R.P.;
"Mutations within the gene encoding the alpha I (X) chain of type
collagen (COL10A1) cause metaphyseal chondrodysplasia type Schmid
not several other forms of metaphyseal chondrodysplasia.";
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Bonaventure J., Chaminade F., Maroteaux P.;
"Mutations in three subdomains of the carboxy-terminal region of collagen type X account for most of the Schmid metaphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94272470; PubMed=8004099; McIntosh I., Abbott M.H., Marman M.L., Olsen B.R., Francomano C "Additional mutations of type X collagen confirm COL10A1 as the Schmid metaphyseal chondrodysplasia locus."; Hum. Mol. Genet. 3:303-307(1994).
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Nakamura Y.;
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MEDLINE=99057503; PubMed=9837818;
Mishimura G., Nagai T.,
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Hum. Mutat. 9:131-135(1997).
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MEDLINE=97220591; PubMed=9067753;
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"Mutations in
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PubMed=7607655;
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ly in vitro is prevented by a Gly618
) NC1 domain resulting in Schmid
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MIM; 120110; -.
MIM; 156500; -.
MIM; 184250; -.
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Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cartilage; Collagen; Signal; Disease mutation; Polymorphism.

Cartilage; Collagen; Signal; Disease mutation; Polymorphism.

1 18 POTENTIAL.
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InterPro; IPR000087; Collagen.
Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RADIOGRAPHY USUALLY SHOWS SCLEROSIS OF THE RIBS, FLARING OF THE METAPHYSES, AND A WIDE IRREGULAR GROWTH PLATE, ESPECIALLY OF THE KNIES.

KNIES.

10 SEPECTS IN COLIOAL ARE THE CAUSE OF SPONDYLOMETAPHYSEAL DYSPLASIA (SWD). SND COMPRISES A HETEROGENEOUS GROUP OF HERITABLE SKRIETAL DYSPLASIAS CHARACTERIZED BY MODIFICATIONS OF THE SKRIETAL BODIES OF THE SPINE AND METAPHYSES OF THE TUBULAR BONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS SIMILARITY: CONTAINS 1 C1Q DOMAIN.
GPAGLPGPRGPPGPPGIPGPAG---ISVPGKPGQQGPTGAPGPRGFPGEKGAPGVPGMNG
                           TSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG-PGSFG
                                                                                     PRG---
                                                      PRGHPGPSGPPGKPGYGSPGLQGEPGLPGPPGPSAVGKPGVPGLPGKPGERGPYGPKGDV
                                                                                                                                                                                                                                                                                                                                                                                                S; PR00007; COMPLEY; SM00110; C1Q; 1.
TE; PS01113; C1Q; 1
                                                                                                                57;
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                   19
520
545
                                                                                  -GAVPRKP------DPTSNA 211
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMNICIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COL10A1
                                                                                                                                                                                                                                                                                   680
680
680
680
                                                                                                                                                                                                              545
5
                                                                                                                                                                                    591
                                                                                                                           7.6%;
                                                                                                              13;
                                                                                                           Score 140; DB
Pred. No. 0.03
13; Mismatches
                                                                                                                                                               G -> R.

/FTId=VAR_001840.

C -> R (IN SMCD).

/FTId=VAR_001841.
                                                                                                                                                                                                                                                                                    CTO.
                                                                                                                                                                                                                                                                                                                NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
                                                                                                                                                                                                                                        G -> E (IN SMCD).
/FTId=VAR 001838.
G -> R (IN SMCD).
                                                                                                                                                                                                                                                                                                   NONHELICAL REGION
                                                                                                                                                                                                                                                                                                                                            COLLAGEN ALPHA 1(X)
                                                                                                                                                                                                                          /FTId=VAR_001839
                                                                                                                           DB 1
                                                                                                                                       <u>..</u>
                                                                                                                84;
                                                                                                                                       Length 680;
                                                                                                                                                                                                                                                                                                                                              CHAIN.
                                                                                                                Indels
                                                                                                                42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collaboration -
                                                                                                              Gaps
                            270
                                                      129
 186
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8
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CAC2_HA
RESULT 47
CA18_MOUSE
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                                                                                                                                                           片
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                                                                                                                                                                                                                                                                                                                                                                                              A PRODUCTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
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                                                                              밁
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAC2 HAECO
P16252;
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                 Cuticle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J04670; AAA29172.1; -. InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shamansky L.M., Pratt D., Boisvenue R.J., Cox G.N., "Cuticle collagen genes of Haemonchus contortus and elegans are highly conserved.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Trichostrongyloidea; Haemonch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
15-UWN-2002 (Rel. 41, Last annotation
Cuticle collagen 2C (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90136718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemonchus
                                                                                                                                                           110
                                                                                                                                                                                                                                                                          176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDP--TSNATSRGAEGPLPPPSMPAVAGAAG
                                                                                156
                                                                                                                   290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271
                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Parasitol. 37:73-86(1989).

FUNCTION: NEWATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.

BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.

REGIONS, WHICH CONTAIN GLYCINE AS EVERY THIRD AMINO ACID.

MISCELLANGOUS: THE FOLYPETIDE COLLAGENS, THE POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-LINKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE CUTICULAR COLLAGEN FAMILY.
                                                                                                                                                                                              GLALLLIGVAGAGGAMCWRRRRAKPSESRHPG----PGSFGRGGSLGLGGGGGMGPREAE 289
                                                                                PGEKGPRGQDGHPGAP-
                                                                                                                                                                                                                                     IPIPPCKPCPQGRPGPPGPIGPPGEPGTPGNPGAPGNDAPPGPPGPKGPPGPPGKAGAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGEMGPIGPPGPQGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKGEMGYGAPG-----RPGERGLPGPQGPTGPSGPPGVGKRGENGVPGQPGIKGDRGF
                                                                                                                 PGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dasod--dodoniana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGGSLGLGGGGGMGPREAEPGELGIALRGG--GAADPP-----FCPHYEKVSGDYGH
                                                                                                                                                                                                                                                                                                                    50,
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 Connective tissue; Repeat; Multigene family; Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contortus (Barber pole worm).
Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
ngyloidea; Haemonchidae; Haemonchinae; Haemonchus.
                                                                                                                                                                                                                                                                                                                                                                                              210 AA;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=2615789;
                                                                                                                                                                                                                                                                                                                                                                                              19562 MW;
                                                                                                                                                                                                                                                                                                                                31.1%;
                                                                                                                                                                                                                                                                                                                                                     7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334
                                                                                                                                                                                                                                                                                                               <u>ن</u>
                                                                                                                                                                                                                                                                                                               Score 139.5;
Pred. No. 0.01
5; Mismatches
                                                                                                                                                         PSEPLVPGPPGPPGPTGPEGPPGPNGAPGHPGAPGA
                                                                                                                                                                                                                                                                                                                                                                                              E15FAA9A2DF3D74B CRC64;
                                                                                -GNAGHPGQPGQPGPP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                     J.011;
75;
                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                   330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Caenorhabditis
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                       210;
                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in no
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                     109
                                                                                                                                                                                                                                                                          233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                  ū
    ProDom; PD000007; Collagen; 1.
ProDom; PD002078; Fib collagen C;
SMART; SM00038; CLDEF; 1.
SMART; SM000282; LamG; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA1B_MOUSE
                                                                                                                 Pfam; PF01410; COLFI;
Pfam; PF02210; TSPN;
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Ninomiya Y., Oxford J.T., Morris N.P., Andrikopoulos K., Ramirez F., Wardell B.B., Lifferth G.D., Teuscher C., Woodward Taylor B.A., Seegmiller R.E., Olsen B.R.;
"A fibrillar collagen gene, Colllal, is essential for skeletal morphogenesis";
Coll 80:423-430(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95163095; PubMed=7859283; MEDLINE=95163095; PubMed=7859283;
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=96015067; PubMed=8530046; Yoshioka H., Inoguchi K., Khaleduzzaman M., Andrikopoulos K., Ramirez F.; "Coding sequence and alternative splicing of collagen gene (Collial)."; Genomics 28:337-340(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                061245; Q64047; (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) collagen alpha 1(XI) chain precursor. COLLIAL.
                               InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib collagen_C.
InterPro; IPR001791; LamInin_G.
InterPro; IPR001130; Prenyl_Site.
InterPro; IPR003129; TSPN.
                                                                                                                                                                                                                                EMBL; D38162;
EMBL; S74574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                    send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND TRACHEA.
SIMILARITY: BELONG
SIMILARITY: HIGH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: TRINERS COMPOSED OF THEE DIFFERENT CHAINS: ALPHA 1(XI), ALPHA 2(XI), AND ALPHA 3(XI), ALPHA 3(XI) ALPHA 1(XI) APPA 2(XI), AND ALPHA 3(XI), ALPHA 1(XI) A POST-TRANSLATIONAL MODIFICATION OF ALPHA 1(II), ALPHA 1(V) CAN ALSO BE FOUND INSTEAD OF ALPHA 3(XI)=1(II) (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 2 ISOFORMS, A LONG FORM (SHOWN HERE) AND A SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.

SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.

PIW: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING PIW: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE CHAINS.

DISEASE: DEFECTS IN COLLIAL ARE ASSOCIATED MITH CHONDRODYSPLASIA, AN AUTOSOMAL RECESSIVE DISEASE CHARACTERIZED BY SKELETAL DEFECTS

CAUSED BY AENORMALITIES IN THE CARTILAGE OF LIMBS, RIBS, MANDIBLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 80:423-430(1995).
FUNCTION: MAY PLAY AN IMPORTANT ROLE IN FIBRILLOGENESIS
CONTROLLING LATERAL GROWTH OF COLLAGEN II FIBRILS.
                                                                                                                                                                                                    MGI:88446; Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181-198 FROM N.A.,
                                                                                                                                                                                                                            BAA07367.1; -.
AAB33439.1; -.
Collagen; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BELONGS TO THE FIBRILLAR CLASS OF COLLAGENS. HIGH, TO ALPHA 1(V) AND ALPHA 3(V) CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND CHONDRODYSPLASIA VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1804
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Connective tissue; Repeat; Hydroxylation;

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RESULT 48
CA12_MOUSE
ID CA12_M
AC P28481
AC P28481
AC P28481
DT 01-DEC
DT 01-DEC
DT 16-OCT
DE CO11ag
GN CO12A1
OS Mus mu
OC Eukary
OC Eukary
OC Mammal
OX NCBI T
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Best Local :
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=91358489; PubMed=1885613;
MetBaranta M., Toman D., de Crombrughe B.,
MetBaranta F. Toman B., Complete nucle
"Mouse type II collagen gene. Complete nucle
structure, and alternative splicing.";
- "ial. Chem. 266:16862-16869(1991)."
                                                                                                                                                                                                                                              -CA12 MOUSE
P28481;
01-DEC-1992
01-DEC-1992
16-OCT-2001
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Disease mutati
SIGNAL
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VARSPLIC
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DOMAIN
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                    KGPQGKPGLAGLPGADGPPGHPGKEGQSGEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CROSSLINKING.
CROSSLINKING.
MISSING (IN SHORT ISOFORM).
LDRSERS -> SIEVRDR (IN CHONDRODYSPLASIA).
MISSING (IN CHONDRODYSPLASIA).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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COLLAGEN ALPHA 1(XI) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRIPLE-HELICAL REGION.
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                                                                                                                                                                                                                                                                                                                   1459
                                                                                                                                                                                                                                                                                                                                                                                                    ----ALGPPGPQGP
                                                               nucleotide sequence,
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                                                                                                                                                                                                                                                                                                                 AA
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                                                                                   Vuorio E.;
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                              RESULT 49
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Query Match
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InterPro; IPR000085; Fib_collagen_C
InterPro; IPR000085; Fib_collagen_C
InterPro; IPR000085; Fib_collagen_C
Pfam; PF00003; VVC; 1
Pfam; PF0139; Collagen; 18.
Pfam; PF01410; COLFI; 1.
ProDom; PD002070; Collagen; 3.
ProDom; PD002070; Collagen; 3.
ProDom; PD002070; Fib_collagen_C; 1
SMART; SM00038; COLFI; 1.
SMART; SM000314; VWC; 1.
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VARSPLIC
SEQUENCE
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- FUNCTION: COLLAGO TYPE II IS SPECIFIC FOR CARTHAGINOUS TISSUES
-I- SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(II) CHAINS.
-I- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-I- SIMILARITY: CONTAINS 1 VMFC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Cartilage; Signal; Alternative splicing. SIGNAL 1 25 POTENTIAL
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SEQUENCE OF 1455-1459 FROM N.A.
MEDLINE=91274355; PubMed=2054384;
Metsarata M., Toman D., de Crombi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M65161; AAA68100.1; -. EMBL; X57982; CAA41047.1; -.
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MGD; MGI:88452; Col2al.
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634
                                                                              580
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                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                    GGMGPREAEPGELGIA----LRG-----GGAADPPFCPHYEKVSGDYGHPVYIVQDGP
  SGFQGLPGPPGPP
                                                                                                                                                               EPGLPGARG:
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                                                                              KGANGEPGKAGEKGLAGAPGLRGLPGKDGETGAAGPPGPSGPAGERGEQGAP-
                                        44SQ4----PQSPP
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1459
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                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                         Score 138.5; D
Pred. No. 0.09;
                                                                                                                                                                                                                                                                                                                                                                                                     NONHELICAL REGION (C-TERMINAL).
Q -> R (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
M; F6C84FA7C532E7F2 CRC64;
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CARBOXYL-TERMINAL PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHONDROCALCIN).
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                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROPERTIDE
                                                                                                                                                                                                                                                                                                                        75;
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Melkoniemi M., Brunner H.G., Manouvrier S., Hennekam R., Superti-Furga A., Kaeaeriaeinen H., Pauli R.M., van Essen T., Warman M.L., Bonaventure J., Miny P., Ala-Kokko L.; "Autosomal recessive disorder otospondylomegaepiphyseal dysplasia associated with loss-of-function mutations in the COL11A2 gene."; Am. J. Hum. Genet. 66:368-377(2000).
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SEQUENCE
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P13942; Q13273; Q13271; Q13272; Q07751;
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence upda
15-JUN-2002 (Rel. 41, Last annotation up
Collagen alpha 2(XI) chain precursor.
MEDLINE=97255959; PubMed=9101290;
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"Mutations in fibrillar collagens (types I, II, III
associated collagen (type IX), and network-forming
cause a spectrum of diseases of bone, cartilage, ar
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Alternative mRNA pro-alpha 1(XI) ar J. Biol. Chem. 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lui V.C., Ng L.J., Sat E.W., Cheah K.S.;
"The human alpha 2(XI) collagen gene (COL11A2): completion of coding information, identification of the promoter sequence, and precise localization within the major histocompatibility complex reveal overlap with the KE5 gene.";
Genomics 32:401-412(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         localization overlap with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89340485; PubMed=2760050; Kimura T., Cheah K.S.E., Chan S.D.H., Lui V.C.H., Mattei M.-G., Kimura T., Cheah K.S.E., Chan S.D.H., Ninomiya Y., Olsen B.R.; van der Reet M., Ono K., Solomon E., Ninomiya Y., Olsen B.R.; "The human alpha 2(XI) collagen (COL11A2) chain. Molecular cloning of "The human alpha 2(XI) collagen (COL11A2) chain. Molecular cloning of CDNA and genomic DNA reveals characteristics of a fibrillar collagen with differences in genomic organization."; J. Biol. Chem. 264:13910-13916(1989).
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Ala-Kokko L.;
Ala-Kokko L.;
COL11A2 gene
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                          PubMed=10677296;
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with the genes for the major
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Justice S.K., Mayn
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RNA processing occurs in the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the value of the valu
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hlajamaa T., Vandenberg
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or fibrillar collagens.";
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  III, and XI), fibri
ing collagen (type )
, and blood vessels.
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otospondylomegaepiphyseal dysplasia accompanied by severe hearing loss.

syndrome. DISEASE: Defects in

COL11A2 are the

cause of autosomal recessive (OSMED), a skeletal dysplasia The phenotype overlaps that

lasia hat of

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MEDLINE 20047768; PubMed=10581026;

A McGuirt W.T., Prasad S.D., Griffith A.J., Kunst H.P.M., Green G.E.,

A Shpargel K.B., Runge C., Huybrechte C., Mueller R.F., Lynch E.,

RA Arita M., Mayne R., Prockop D.J., Van Camp G., Smith R.J.H.;

RY "Mutations in COLLIAS cause non-syndromic hearing loss (DFNA13).";

RI Nat. Genet. 23:413-419(199)

C. I- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN FIBRILS.

C. I- SUBUNIT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1(XI),

ALPHA 2(XI), AND ALPHA 3(XI) ALPHA 3(XI) IS A POST-FRANSLATIONAL

C. MODIFICATION OF ALPHA 1(II). ALPHA 3(XI) IS A POST-FRANSLATIONAL

C. MODIFICATION OF ALPHA 1(II). ALPHA 1(V) CAN ALSO BE FOUND INSTEAD

OF ALPHA 3(XI)=1(II).

C. I- ALTERNATIVE PRODUCTS: 8 isoforms; 1 (shown here), 2, 3, 4, 5, 6, 7

C. and 8; may be produced by alternative splicing. They lack exons 6,

C. I- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING

C. I- PTM: A DISULFIDE-BONDED PEPTIDE CALLED PROLINE ARGINING THE GRAINS.

C. I- PTM: A DISULFIDE-BONDED PEPTIDE CALLED PROLINE ARGINING THE CHAINS.

C. CARTILAGE MATRIX FROM WHICH IT CAN BE ISOLATED IN SIGNIFICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giedion A., Wiesbauer P., Spranger J., Winterpacht A., Zabel B., "Heterozygous glycine substitution in the COL11A2 gene in the origatient with the Weissenbacher-Zweymueller syndrome demonstrates identity with heterozygous OSMED (nonocular Stickler syndrome).", Am. J. Med. Genet. 80:115-120(1998).
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VARIANTS DENAI3 GLU-808 AND CYS-1034,
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PubMed=9506662;
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AMOUNTS.

DISEASE: Defects in COLILA2 are the cause of Stickler syndrome type 3 (STL3). It is an autosomal dominant disorder characterized by oro-facial, auditory and skeletal manifestations, such as midfacial hypoplasia, cleft palate, osteoarthritis, and sensorineural hearing loss. Differently from Stickler syndrome type 1 and 2, no ocular involvement is observed. This disorder is also referred to as Stickler-like syndrome or non-ocular Stickler
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an E.C.M., Lui V.C.
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Matches 64
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InterPro; IPR000885; Fib collagen.C.
InterPro; IPR001291; Laminin.G.
InterPro; IPR001230; Prenyl_Site.
InterPro; IPR001230; Prenyl_Site.
InterPro; IPR003129; TSPN.
Pfam; PP01391; Collagen; 18.
Pfam; PP01410; COLPI; 1.
Pfam; PP01410; COLPI; 1.
Pfam; PP01410; TSPN; 1.
Pfam; PP0000077; Collagen; 1.
ProDom; PD0000078; Fib_collagen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32169; AAC50214.1; -.
EMBL; U32169; AAC50213.1; -.
EMBL; U32169; AAC50215.1; -.
EMBL; AL031228; CAA20240.1; -.
EMBL; L18987; AAA35498.1; -.
EMBL; U49974; AAA52034.1; -.
EMBL; U41069; AAC17464.1; JOINED.
EMBL; U41066; AAC17464.1; JOINED.
EMBL; U41066; AAC17464.1; JOINED.
EMBL; U41067; AAC17464.1; JOINED.
EMBL; U41067; AAC17464.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000007; Collagen; 1.
ProDom; PD002078; Fib collagen_C;
SMART; SM00038; COLFI; 1.
SMART; SM000282; LamG; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DISEASE: Defects in COLIIA2 are the cause of Meissenbacher-
Zweymueller syndrome (MZS), an autosomal dominant disorder allelic with STL3 and OSMED. It is also referred to as heterozygous OSMED.

DISEASE: Defects in COLIIA2 are the cause of autosomal dominant nonsyndromic sensorineural dathess type 13 (DPNA13). Affected individuals experience progressive hearing loss beginning in the second to fourth decades, eventually making use of amplification making use of amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATCHESCULY:
SIMILARITY: BELONGS TO THE FIBRILLAR CLASS OF COLLAGENS
DATABASE: NAME=Hereditary hearing loss homepage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE=Gene page;
WWW="http://www.uia.ac.be/dnalab/hhh/hhhgenes.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A32645; A32645
W; HGNC:2187; CC
HYEK-VSGDYGHPVYIVQDGPP
                                                                                                                                                                                                                                      GLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK--PVSEMPMERDRGAAHSLEPGKENLP 204
                                                                                                                                                               GDPTS----NATSR-GAEGPLPPPSMPAVAGAAGGLALL---
                                                                                                                                                                                                   GSEGRQGG----KGAK-----GDPGAIGAPGKTGPVGP----AGPAGKPGPDGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184840;
                                                 -EQGEKGDRGLPGPQGSPGQKGEMGIPGASGPIGP-GGPPGLPGPAGPKGAKGATGPGGP
                                                                                                                            GLPGSVGQQGRPGATGQAGPPGPVGPPGLPGLRGDAGAKGEKGHPGLIGLIGPPG-----
                                                                                    RRRAKPSESRHPGP-GSFGRGGSLGL-GGGGGMGPREAEPGELGIA-LRGGGAADPPFCP
                                                                                                                                                                                                                                                                            64;
                                                                                                                                                                                                                                                                                               Similarity
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31.7%;
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                                                                                                                                                               -LLGVAGAGGAMCWR
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CA24_CAEEL STANDARD
F17140; Q19098; Q19099;
This SWISS-PROT entry is copyright. It is produced through a clearly between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (Rel. 15, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Collagen alpha 2(IV) chain precursor (Lethal LET-2 OR CLB-1 OR F01G12.5.
Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda; Chromadorea, Rh
Rhabditidae, Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                Sibley M.H., Graham P.L., von Mende N., Kramer J.M.; "Mutations in the alpha 2(IV) basement membrane collagen gene of Caenorhabditis elegans produce phenotypes of differing severities."; EMBO J. 13:3278-3285(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sibley M.H., Johnson J.J., Mello C.C., Kramer J.M.; "Genetic identification, sequence, and alternative Caenorhabditis elegans alpha 2(IV) collagen gene."; J. Cell Biol. 123:255-264(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1482
                                                                                                                                                                                                                                                                                                               -i- FUNCTION: Collagen type IV is specific for basement membranes.
Vital for embronic development.
-i- SUBUNIT: TRIMERS OF TWO ALPHA 1(IV) AND ONE ALPHA 2(IV) CHAIN.
TYPE IV COLLAGEN FORMS A MESH-LIKE NETWORK LINKED THROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94320591;
                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The two Caenorhabditis elegans basement membrane (type IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94012964; PubMed=7691828;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are located on separate chromosomes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (APR-1996)
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Best Local Similarity 29.4%;
Matches 64; Conservative 1
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EMBL; Z22964; CAA80537.1; -.
EMBL; J05066; AAA27989.1; -.
EMBL; U22327; AAA6431Z.1; ALT_SEQ.
EMBL; U53342; AAA96215.1; -.
EMBL; U53342; AAA96216.1; -.
EMBL; U533
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WormPep; F01G12.5b; CE04335.
InterPro; IPR001087; C01lagen.
InterPro; IPR001442; ProcollagnC4.
Pfam; PF01391; C01lagen; 23.
Pfam; PF01413; C4; 2.
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ProDom; PD003923; ProcollagnC4; 2.
SMART; SM00111; C4; 2.
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Alternative spl
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                                               LGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPP 330
                                                                                                       TGLPGYG----
                                                                                                                                                     LGVAGAGGAMCWRRRRAKPSESRHPG-PGSFGRGGSL-----GLGGGGGMGPREAEPGE 292
                                                                                                                                                                                                                                                    -----AAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 239
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NONHELICAL REGION (NC1).
NOR 1632 (BY SIMILARITY).
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OR 1747 (BY SIMILARITY).
BY SIMILARITY.
OR 1750 (BY SIMILARITY).
OR 1750 (BY SIMILARITY).
BY SIMILARITY.
OLINEED (GLYCOSAMINOGLYCAN) (POTENTIAL).
GDLGSVGPPGPPGPFFTGSGSIVGPRGNFGEKGDK -> G
DJGAMGPAGPPGPTASTMSKGTTIGFKGDLGEKGEK (IN
                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 138; DB 1; Length 1758;
Pred. No. 0.12;
2; Mismatches 76; Indels 6
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COLLAGEN ALPHA 2(IV) CHAIN.
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    L (IN REF. 1 AND 3; AAA96216).
    97EE3F3DBB2D2AC5.CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E (IN MN114; 73% LETHAL).

E (IN MN126; 100% LETHAL).

E (IN MN109; 37% LETHAL).

R (IN MN103 AND MN151; 96% LETHAL).

R (IN MN101; 100% LETHAL).

E (IN MN102; 50% LETHAL).

E (IN MN129; 100% LETHAL).

E (IN MN129; 100% LETHAL).

E (IN MN139; 100% LETHAL).

R (IN G30; 90% LETHAL).

R (IN G30; 90% LETHAL).

R (IN G30; 90% LETHAL).

B (IN MN139; 20% LETHAL).

D (IN MN19; 20% LETHAL).

D (IN MN147; 7% LETHAL).

D (IN MN147; 7% LETHAL).

D (IN MN147; 7% LETHAL).
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Search completed: February 11, 2003, 12:03:55 Job time : 25.5409 secs